

SEQUENCE LISTING

<110> Andre R. Abad
 Ronald D. Flannagan
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 Albert L. Lu
 Billy Fred McCutchen
 James K. Presnail
 James F.H. Wong
 Cao-Guo Yu

<120> Genes Encoding Proteins With Pesticidal
 Activity

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3621

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115 120 125

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Thr Thr Thr Ile Asn Asn Tyr Tyr Asp Arg Gln Met Lys Leu Thr Ala	
225 230 235 240	
gaa tat tct gat cac tgt gta aag tgg tat gaa act ggt tta gca aaa	768
Glu Tyr Ser Asp His Cys Val Lys Trp Tyr Glu Thr Gly Leu Ala Lys	
245 250 255	
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Leu Lys Gly Thr Ser Ala Lys Gln Trp Val Asp Tyr Asn Gln Phe Arg	
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Arg Glu Met Thr Leu Thr Val Leu Asp Val Val Ala Leu Phe Pro Asn	
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Tyr Asp Thr Arg Thr Tyr Pro Met Glu Thr Lys Ala Gln Leu Thr Arg	
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Ile Arg Pro Pro His Val Phe Asp Tyr Ile Thr Gly Leu Thr Val Tyr	
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Thr Gln Ser Arg Ser Ile Ser Ser Ala Arg Tyr Ile Arg His Trp Ala	
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Gly His Gln Ile Ser Tyr His Arg Ile Phe Ser Asp Asn Ile Ile Lys	
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Gln Met Tyr Gly Thr Asn Gln Asn Leu His Ser Thr Ser Thr Phe Asp	
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Phe Thr Asn Tyr Asp Ile Tyr Lys Thr Leu Ser Lys Asp Ala Val Leu	
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tta aag tat aat ccg gtt tcc aaa gat att ata gcg ggg aca aga gat Leu Lys Tyr Asn Pro Val Ser Lys Asp Ile Ile Ala Gly Thr Arg Asp 450 455 460			1392
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tca tat agc cat aga tta tgt cat atc aca agt att ccc gcg acg ggt Ser Tyr Ser His Arg Leu Cys His Ile Thr Ser Ile Pro Ala Thr Gly 485 490 495			1488
tca act acc gga tta gta cct gta ttt tct tgg aca cat cgg agt gcc Ser Thr Thr Gly Leu Val Pro Val Phe Ser Trp Thr His Arg Ser Ala 500 505 510			1536
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675 680 685	
aat aca aaa gat ggc tta cga cca ggc gta acg gat tat gaa gtg aat	2112
Asn Thr Lys Asp Gly Leu Arg Pro Gly Val Thr Asp Tyr Glu Val Asn	
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785 790 795 800	
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Ser Gln Gly Leu Glu Ile Phe Thr Ile Arg His Gln Thr Asn Arg Ile	
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Val Lys Asn Val Pro Asp Asp Leu Leu Pro Asp Val Ser Pro Val Asn	
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Arg Leu Glu Val Glu Asn Arg Ser Gly Glu Ala His Glu Phe Ser Ile	
865 870 875 880	

cct att gat aca ggt gaa atc gat tac aat gaa aat gca gga ata tgg	2688
Pro Ile Asp Thr Gly Glu Ile Asp Tyr Asn Glu Asn Ala Gly Ile Trp	
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Tyr Asn Glu Met Phe Pro Glu Ile Pro Gly Met Asn Tyr Thr Lys Phe	
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Val Gly Asn Gly Tyr Val Ser Ile Arg Asp Gly Gly Asn Gln Thr Glu	
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 Pro Ile Asp Thr Gly Glu Ile Asp Tyr Asn Glu Asn Ala Gly Ile Trp
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Asp Gln Thr Gly Tyr Ile Thr Lys Thr Val Thr Phe Ile Pro Tyr Thr		
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Pro Thr Asn Ala Leu Gln Asn Met Asp Tyr Lys Asp Tyr Leu Lys Met	
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Ser Ala Gly Asn Ala Ser Glu Tyr Pro Gly Ser Pro Glu Val Leu Val	
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Glu Tyr Ala Arg Asn Lys Ala Leu Ser Glu Leu Glu Gly Leu Gly Asn	
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Glu Tyr Ser Asp His Cys Val Lys Trp Tyr Glu Thr Gly Leu Ala Lys	
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Tyr Asp Thr Arg Thr Tyr Pro Met Glu Thr Lys Ala Gln Leu Thr Arg	
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Ser Trp Tyr Asp Lys Ala Pro Ser Phe Gly Val Ile Glu Ser Ser Val	
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Ser Gly Gln Asp Ala Ala Lys Ala Ala Ile Asp Ile Val Gly Lys Leu																			
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Glu	Val	Pro	Phe	Leu	Thr	Val	Tyr	Ala	Met	Ala	Ala	Asn	Leu	His	Leu	
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Leu	Leu	Leu	Lys	Asp	Ala	Ser	Ile	Phe	Gly	Glu	Glu	Trp	Gly	Trp	Ser	
210						215					220					
Thr	Thr	Thr	Ile	Asn	Asn	Tyr	Tyr	Asp	Arg	Gln	Met	Lys	Leu	Thr	Ala	
225				230						235					240	
Glu	Tyr	Ser	Asp	His	Cys	Val	Lys	Trp	Tyr	Glu	Thr	Gly	Leu	Ala	Lys	
				245					250					255		
Leu	Lys	Gly	Thr	Ser	Ala	Lys	Gln	Trp	Val	Asp	Tyr	Asn	Gln	Phe	Arg	
			260					265					270			
Arg	Glu	Met	Thr	Leu	Ala	Val	Leu	Asp	Val	Val	Ala	Leu	Phe	Pro	Asn	
		275					280					285				
Tyr	Asp	Thr	Arg	Thr	Tyr	Pro	Met	Glu	Thr	Lys	Ala	Gln	Leu	Thr	Arg	
290					295						300					
Glu	Val	Tyr	Thr	Asp	Pro	Leu	Gly	Ala	Val	Asn	Val	Ser	Ser	Ile	Gly	
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Ser	Trp	Tyr	Asp	Lys	Ala	Pro	Ser	Phe	Gly	Val	Ile	Glu	Ser	Ser	Val	
				325					330					335		
Ile	Arg	Pro	Pro	His	Val	Phe	Asp	Tyr	Ile	Thr	Gly	Leu	Thr	Val	Tyr	
			340					345					350			
Thr	Gln	Ser	Arg	Ser	Ile	Ser	Ser	Ala	Arg	Tyr	Ile	Arg	His	Trp	Ala	
		355					360					365				
Gly	His	Gln	Ile	Ser	Tyr	His	Arg	Val	Ser	Arg	Gly	Ser	Asn	Leu	Gln	
370					375						380					
Gln	Met	Tyr	Gly	Thr	Asn	Gln	Asn	Leu	His	Ser	Thr	Ser	Thr	Phe	Asp	
385					390					395					400	
Phe	Thr	Asn	Tyr	Asp	Ile	Tyr	Lys	Thr	Leu	Ser	Lys	Asp	Ala	Val	Leu	
				405					410					415		
Leu	Asp	Ile	Val	Tyr	Pro	Gly	Tyr	Thr	Tyr	Ile	Phe	Phe	Gly	Met	Pro	
			420					425					430			
Glu	Val	Glu	Phe	Phe	Met	Val	Asn	Gln	Leu	Asn	Asn	Thr	Arg	Lys	Thr	
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Ser	Glu	Leu	Glu	Leu	Pro	Pro	Glu	Thr	Ser	Asp	Gln	Pro	Asn	Tyr	Glu	
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				485					490					495		
Asn	Thr	Thr	Gly	Leu	Val	Pro	Val	Phe	Ser	Trp	Thr	His	Arg	Ser	Ala	
				500				505					510			
Asp	Leu	Asn	Asn	Thr	Ile	Tyr	Ser	Asp	Lys	Ile	Thr	Gln	Ile	Pro	Ala	
		515					520					525				
Val	Lys	Cys	Trp	Asp	Asn	Leu	Pro	Phe	Val	Pro	Val	Val	Lys	Gly	Pro	
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Gly	His	Thr	Gly	Gly	Asp	Leu	Leu	Gln	Tyr	Asn	Arg	Ser	Thr	Gly	Ser	
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Val	Gly	Thr	Leu	Phe	Leu	Ala	Arg	Tyr	Gly	Leu	Ala	Leu	Glu	Lys	Ala	
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gaa tat gca agg aat aaa gcg ctt tcg gaa tta gaa gga tta ggt aat			432
Glu Tyr Ala Arg Asn Lys Ala Leu Ser Glu Leu Glu Gly Leu Gly Asn			
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aat tac caa tta tat cta act gcg ctt gaa gaa tgg gaa gaa aat cca			480
Asn Tyr Gln Leu Tyr Leu Thr Ala Leu Glu Glu Trp Glu Glu Asn Pro			
145	150	155	160
aat ggt tca aga aat ggt tcc cgg gcc tta cga gat gtg cga aat cga			528
Asn Gly Ser Arg Asn Gly Ser Arg Ala Leu Arg Asp Val Arg Asn Arg			
	165	170	175
ttt gaa atc ctg gat agt tta ttt acg caa tat atg cca tct ttt aga			576
Phe Glu Ile Leu Asp Ser Leu Phe Thr Gln Tyr Met Pro Ser Phe Arg			
	180	185	190
gtg aca aat ttt gaa gta cca ttc ctt act gta tat gca atg gca gcc			624
Val Thr Asn Phe Glu Val Pro Phe Leu Thr Val Tyr Ala Met Ala Ala			
	195	200	205
aac ctt cat tta ctg tta tta aag gac gcg tca att ttt gga gaa gaa			672
Asn Leu His Leu Leu Leu Leu Lys Asp Ala Ser Ile Phe Gly Glu Glu			
	210	215	220
tgg gga tgg tca aca act act att aat aac tat tat gat cgt caa atg			720
Trp Gly Trp Ser Thr Thr Thr Ile Asn Asn Tyr Tyr Asp Arg Gln Met			
	225	230	235
aaa ctt act gca gaa tat tct gat cac tgt gta aag tgg tat gaa act			768
Lys Leu Thr Ala Glu Tyr Ser Asp His Cys Val Lys Trp Tyr Glu Thr			
	245	250	255
ggt tta gca aaa tta aaa ggc acg agc gct aaa caa tgg gtt gac tat			816
Gly Leu Ala Lys Leu Lys Gly Thr Ser Ala Lys Gln Trp Val Asp Tyr			
	260	265	270
aac caa ttc cgt aga gaa atg aca ctg gcg gtt tta gat gtt gtt gca			864
Asn Gln Phe Arg Arg Glu Met Thr Leu Ala Val Leu Asp Val Val Ala			
	275	280	285
tta ttc cca aat tat gac aca cgc acg tac cca atg gaa acg aaa gca			912
Leu Phe Pro Asn Tyr Asp Thr Arg Thr Tyr Pro Met Glu Thr Lys Ala			
	290	295	300
caa cta aca agg gaa gta tat aca gat cca ctg ggc gcg gta aac gtg			960
Gln Leu Thr Arg Glu Val Tyr Thr Asp Pro Leu Gly Ala Val Asn Val			
	305	310	315
tct tca att ggt tcc tgg tat gac aaa gca cct tct ttc gga gtg ata			1008
Ser Ser Ile Gly Ser Trp Tyr Asp Lys Ala Pro Ser Phe Gly Val Ile			
	325	330	335
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Glu Ser Ser Val Ile Arg Pro Pro His Val Phe Asp Tyr Ile Thr Gly			
	340	345	350

ctc aca gtg tat aca caa tca aga agc att tct tcc gct cgc tat ata	1104
Leu Thr Val Tyr Thr Gln Ser Arg Ser Ile Ser Ser Ala Arg Tyr Ile	
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aga cat tgg gct ggt cat caa ata agc tac cat cgt gtc agt agg ggt	1152
Arg His Trp Ala Gly His Gln Ile Ser Tyr His Arg Val Ser Arg Gly	
370 375 380	
agt aat ctt caa caa atg tat gga act aat caa aat cta cac agc act	1200
Ser Asn Leu Gln Gln Met Tyr Gly Thr Asn Gln Asn Leu His Ser Thr	
385 390 395 400	
agt acc ttt gat ttt acg aat tat gat att tac aag act cta tca aag	1248
Ser Thr Phe Asp Phe Thr Asn Tyr Asp Ile Tyr Lys Thr Leu Ser Lys	
405 410 415	
gat gca gta ctc ctt gat att gtt tac cct ggt tat acg tat ata ttt	1296
Asp Ala Val Leu Leu Asp Ile Val Tyr Pro Gly Tyr Thr Tyr Ile Phe	
420 425 430	
ttt gga atg cca gaa gtc gag ttt ttc atg gta aac caa ttg aat aat	1344
Phe Gly Met Pro Glu Val Glu Phe Phe Met Val Asn Gln Leu Asn Asn	
435 440 445	
acc aga aag acg tta aag tat aat cca gtt tcc aaa gat att ata gcg	1392
Thr Arg Lys Thr Leu Lys Tyr Asn Pro Val Ser Lys Asp Ile Ile Ala	
450 455 460	
agt aca aga gat tcg gaa tta gaa tta cct cca gaa act tca gat caa	1440
Ser Thr Arg Asp Ser Glu Leu Glu Leu Pro Pro Glu Thr Ser Asp Gln	
465 470 475 480	
cca aat tat gag tca tat agc cat aga tta tgt cat atc aca agt att	1488
Pro Asn Tyr Glu Ser Tyr Ser His Arg Leu Cys His Ile Thr Ser Ile	
485 490 495	
ccc gcg acg ggt aac act acc gga tta gta cct gta ttt tct tgg aca	1536
Pro Ala Thr Gly Asn Thr Thr Gly Leu Val Pro Val Phe Ser Trp Thr	
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cat cga agt gca gat tta aac aat aca ata tat tca gat aaa atc act	1584
His Arg Ser Ala Asp Leu Asn Asn Thr Ile Tyr Ser Asp Lys Ile Thr	
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caa att ccg gcc gtt aaa tgt tgg gat aat tta ccg ttt gtt cca gtg	1632
Gln Ile Pro Ala Val Lys Cys Trp Asp Asn Leu Pro Phe Val Pro Val	
530 535 540	
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Val Lys Gly Pro Gly His Thr Gly Gly Asp Leu Leu Gln Tyr Asn Arg	
545 550 555 560	
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Ser Thr Gly Ser Val Gly Thr Leu Phe Leu Ala Arg Tyr Gly Leu Ala	
565 570 575	

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Leu Glu Lys Ala Gly Lys Tyr Arg Val Arg Leu Arg Tyr Ala Thr Asp	
580 585 590	
gca gat att gta ttg cat gta aac gat gct cag att cag atg cca aaa	1824
Ala Asp Ile Val Leu His Val Asn Asp Ala Gln Ile Gln Met Pro Lys	
595 600 605	
aca atg aac cca ggt gag gat ctg aca tct aaa act ttt aaa gtt gca	1872
Thr Met Asn Pro Gly Glu Asp Leu Thr Ser Lys Thr Phe Lys Val Ala	
610 615 620	
gat gct atc aca aca tta aat tta gca aca gat agt tcg cta gca ttg	1920
Asp Ala Ile Thr Thr Leu Asn Leu Ala Thr Asp Ser Ser Leu Ala Leu	
625 630 635 640	
aaa cat aat tta ggt gaa gac cct aat tca aca tta tct ggt ata gtt	1968
Lys His Asn Leu Gly Glu Asp Pro Asn Ser Thr Leu Ser Gly Ile Val	
645 650 655	
tac gtt gac cga atc gaa ttc atc cca gta gat gag aca tat gaa gcg	2016
Tyr Val Asp Arg Ile Glu Phe Ile Pro Val Asp Glu Thr Tyr Glu Ala	
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gaa taa	2022
Glu *	

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 <212> PRT
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Pro Thr Asn Ala Leu Gln Asn Met Asp Tyr Lys Asp Tyr Leu Lys Met	
35 40 45	
Ser Ala Gly Asn Ala Ser Glu Tyr Pro Gly Ser Pro Glu Val Leu Val	
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Ser Gly Gln Asp Ala Ala Lys Ala Ala Ile Asp Ile Val Gly Lys Leu	
65 70 75 80	
Leu Ser Gly Leu Gly Val Pro Phe Val Gly Pro Ile Val Ser Leu Tyr	
85 90 95	
Thr Gln Leu Ile Asp Ile Leu Trp Pro Ser Gly Glu Lys Ser Gln Trp	
100 105 110	
Glu Ile Phe Met Glu Gln Val Glu Glu Leu Ile Asn Gln Lys Ile Ala	
115 120 125	
Glu Tyr Ala Arg Asn Lys Ala Leu Ser Glu Leu Glu Gly Leu Gly Asn	
130 135 140	
Asn Tyr Gln Leu Tyr Leu Thr Ala Leu Glu Glu Trp Glu Glu Asn Pro	
145 150 155 160	
Asn Gly Ser Arg Asn Gly Ser Arg Ala Leu Arg Asp Val Arg Asn Arg	
165 170 175	

Phe Glu Ile Leu Asp Ser Leu Phe Thr Gln Tyr Met Pro Ser Phe Arg
180 185 190
Val Thr Asn Phe Glu Val Pro Phe Leu Thr Val Tyr Ala Met Ala Ala
195 200 205
Asn Leu His Leu Leu Leu Lys Asp Ala Ser Ile Phe Gly Glu Glu
210 215 220
Trp Gly Trp Ser Thr Thr Thr Ile Asn Asn Tyr Tyr Asp Arg Gln Met
225 230 235 240
Lys Leu Thr Ala Glu Tyr Ser Asp His Cys Val Lys Trp Tyr Glu Thr
245 250 255
Gly Leu Ala Lys Leu Lys Gly Thr Ser Ala Lys Gln Trp Val Asp Tyr
260 265 270
Asn Gln Phe Arg Arg Glu Met Thr Leu Ala Val Leu Asp Val Val Ala
275 280 285
Leu Phe Pro Asn Tyr Asp Thr Arg Thr Tyr Pro Met Glu Thr Lys Ala
290 295 300
Gln Leu Thr Arg Glu Val Tyr Thr Asp Pro Leu Gly Ala Val Asn Val
305 310 315 320
Ser Ser Ile Gly Ser Trp Tyr Asp Lys Ala Pro Ser Phe Gly Val Ile
325 330 335
Glu Ser Ser Val Ile Arg Pro Pro His Val Phe Asp Tyr Ile Thr Gly
340 345 350
Leu Thr Val Tyr Thr Gln Ser Arg Ser Ile Ser Ser Ala Arg Tyr Ile
355 360 365
Arg His Trp Ala Gly His Gln Ile Ser Tyr His Arg Val Ser Arg Gly
370 375 380
Ser Asn Leu Gln Gln Met Tyr Gly Thr Asn Gln Asn Leu His Ser Thr
385 390 395 400
Ser Thr Phe Asp Phe Thr Asn Tyr Asp Ile Tyr Lys Thr Leu Ser Lys
405 410 415
Asp Ala Val Leu Leu Asp Ile Val Tyr Pro Gly Tyr Thr Tyr Ile Phe
420 425 430
Phe Gly Met Pro Glu Val Glu Phe Phe Met Val Asn Gln Leu Asn Asn
435 440 445
Thr Arg Lys Thr Leu Lys Tyr Asn Pro Val Ser Lys Asp Ile Ile Ala
450 455 460
Ser Thr Arg Asp Ser Glu Leu Glu Leu Pro Pro Glu Thr Ser Asp Gln
465 470 475 480
Pro Asn Tyr Glu Ser Tyr Ser His Arg Leu Cys His Ile Thr Ser Ile
485 490 495
Pro Ala Thr Gly Asn Thr Thr Gly Leu Val Pro Val Phe Ser Trp Thr
500 505 510
His Arg Ser Ala Asp Leu Asn Asn Thr Ile Tyr Ser Asp Lys Ile Thr
515 520 525
Gln Ile Pro Ala Val Lys Cys Trp Asp Asn Leu Pro Phe Val Pro Val
530 535 540
Val Lys Gly Pro Gly His Thr Gly Gly Asp Leu Leu Gln Tyr Asn Arg
545 550 555 560
Ser Thr Gly Ser Val Gly Thr Leu Phe Leu Ala Arg Tyr Gly Leu Ala
565 570 575
Leu Glu Lys Ala Gly Lys Tyr Arg Val Arg Leu Arg Tyr Ala Thr Asp
580 585 590
Ala Asp Ile Val Leu His Val Asn Asp Ala Gln Ile Gln Met Pro Lys
595 600 605
Thr Met Asn Pro Gly Glu Asp Leu Thr Ser Lys Thr Phe Lys Val Ala
610 615 620
Asp Ala Ile Thr Thr Leu Asn Leu Ala Thr Asp Ser Ser Leu Ala Leu

625 630 635 640
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<221> misc_feature

<222> (0)...(0)

<223> 1218-1A

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tct act tct gta tcc aat gat tct aac aga tac cct ttt gcg aat gag 96
 Ser Thr Ser Val Ser Asn Asp Ser Asn Arg Tyr Pro Phe Ala Asn Glu
 20 25 30

cca aca aat gcg cta caa aat atg gat tat aaa gat tat tta aaa atg 144

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		35					40					45					
tct	gcg	gga	aat	gct	agt	gaa	tac	cct	ggg	tca	cct	gaa	gta	ctt	gtt	192	
Ser	Ala	Gly	Asn	Ala	Ser	Glu	Tyr	Pro	Gly	Ser	Pro	Glu	Val	Leu	Val		
	50					55					60						
agc	gga	caa	gat	gca	gct	aag	gcc	gca	att	gat	ata	gta	ggg	aaa	tta	240	
Ser	Gly	Gln	Asp	Ala	Ala	Lys	Ala	Ala	Ile	Asp	Ile	Val	Gly	Lys	Leu		
	65				70					75					80		
cta	tca	ggg	tta	ggg	gtc	cca	ttt	gtt	ggg	ccg	ata	gtg	agt	ctt	tat	288	
Leu	Ser	Gly	Leu	Gly	Val	Pro	Phe	Val	Gly	Pro	Ile	Val	Ser	Leu	Tyr		
				85				90						95			
act	caa	ctt	att	gat	att	ctg	tgg	cct	tca	ggg	gaa	aag	agt	caa	tgg	336	
Thr	Gln	Leu	Ile	Asp	Ile	Leu	Trp	Pro	Ser	Gly	Glu	Lys	Ser	Gln	Trp		
			100					105					110				
gaa	att	ttt	atg	gaa	caa	gta	gaa	gaa	ctc	att	aat	caa	aaa	ata	gca	384	
Glu	Ile	Phe	Met	Glu	Gln	Val	Glu	Glu	Leu	Ile	Asn	Gln	Lys	Ile	Ala		
		115					120					125					
gaa	tat	gca	agg	aat	aaa	gcg	ctt	tcg	gaa	tta	gaa	gga	tta	ggg	aat	432	
Glu	Tyr	Ala	Arg	Asn	Lys	Ala	Leu	Ser	Glu	Leu	Glu	Gly	Leu	Gly	Asn		
		130				135						140					
aat	tac	caa	tta	tat	cta	act	gcg	ctt	gaa	gaa	tgg	gaa	gaa	aat	cca	480	
Asn	Tyr	Gln	Leu	Tyr	Leu	Thr	Ala	Leu	Glu	Glu	Trp	Glu	Glu	Asn	Pro		
	145				150					155					160		
aat	ggg	tca	aga	gcc	tta	cga	gat	gtg	cga	aat	cga	ttt	gaa	atc	ctg	528	
Asn	Gly	Ser	Arg	Ala	Leu	Arg	Asp	Val	Arg	Asn	Arg	Phe	Glu	Ile	Leu		
			165					170						175			
gat	agt	tta	ttt	acg	caa	tat	atg	cca	tct	ttt	aga	gtg	aca	aat	ttt	576	
Asp	Ser	Leu	Phe	Thr	Gln	Tyr	Met	Pro	Ser	Phe	Arg	Val	Thr	Asn	Phe		
			180					185					190				
gaa	gta	cca	ttc	ctt	act	gta	tat	gca	atg	gca	gcc	aac	ctt	cat	tta	624	
Glu	Val	Pro	Phe	Leu	Thr	Val	Tyr	Ala	Met	Ala	Ala	Asn	Leu	His	Leu		
		195					200					205					
ctg	tta	tta	aag	gac	gcg	tca	att	ttt	gga	gaa	gaa	tgg	gga	tgg	tca	672	
Leu	Leu	Leu	Lys	Asp	Ala	Ser	Ile	Phe	Gly	Glu	Glu	Trp	Gly	Trp	Ser		
	210					215						220					
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Thr	Thr	Thr	Ile	Asn	Asn	Tyr	Tyr	Asp	Arg	Gln	Met	Lys	Leu	Thr	Ala		
	225				230					235					240		
gaa	tat	tct	gat	cac	tgt	gta	aag	tgg	tat	gaa	act	ggg	tta	gca	aaa	768	
Glu	Tyr	Ser	Asp	His	Cys	Val	Lys	Trp	Tyr	Glu	Thr	Gly	Leu	Ala	Lys		
				245				250						255			
tta	aaa	ggc	acg	agc	gct	aaa	caa	tgg	gtt	gac	tat	aac	caa	ttc	cgt	816	
Leu	Lys	Gly	Thr	Ser	Ala	Lys	Gln	Trp	Val	Asp	Tyr	Asn	Gln	Phe	Arg		

260	265	270	
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Arg Glu Met Thr Leu Ala Val Leu Asp Val Val Ala Leu Phe Pro Asn			
275	280	285	
tat gac aca cgc acg tac cca atg gaa acg aaa gca caa cta aca agg			912
Tyr Asp Thr Arg Thr Tyr Pro Met Glu Thr Lys Ala Gln Leu Thr Arg			
290	295	300	
gaa gta tat aca gat cca ctg ggc gcg gta aac gtg tct tca att ggt			960
Glu Val Tyr Thr Asp Pro Leu Gly Ala Val Asn Val Ser Ser Ile Gly			
305	310	315	320
tcc tgg tat gac aaa gca cct tct ttc gga gtg ata gaa tca tcc gtt			1008
Ser Trp Tyr Asp Lys Ala Pro Ser Phe Gly Val Ile Glu Ser Ser Val			
325	330	335	
att cga cca ccc cat gta ttt gat tat ata acg gga ctc aca gtg tat			1056
Ile Arg Pro Pro His Val Phe Asp Tyr Ile Thr Gly Leu Thr Val Tyr			
340	345	350	
aca caa tca aga agc att tct tcc gct cgc tat ata aga cat tgg gct			1104
Thr Gln Ser Arg Ser Ile Ser Ser Ala Arg Tyr Ile Arg His Trp Ala			
355	360	365	
ggg cat caa ata agc tac cat cgt gtc agt agg ggt agt aat ctt caa			1152
Gly His Gln Ile Ser Tyr His Arg Val Ser Arg Gly Ser Asn Leu Gln			
370	375	380	
caa atg tat gga act aat caa aat cta cac agc act agt acc ttt gat			1200
Gln Met Tyr Gly Thr Asn Gln Asn Leu His Ser Thr Ser Thr Phe Asp			
385	390	395	400
ttt acg aat tat gat att tac aag act cta tca aag gat gca gta ctc			1248
Phe Thr Asn Tyr Asp Ile Tyr Lys Thr Leu Ser Lys Asp Ala Val Leu			
405	410	415	
ctt gat att gtt tac cct ggt tat acg tat ata ttt ttt gga atg cca			1296
Leu Asp Ile Val Tyr Pro Gly Tyr Thr Tyr Ile Phe Phe Gly Met Pro			
420	425	430	
gaa gtc gag ttt ttc atg gta aac caa ttg aat aat acc aga aag acg			1344
Glu Val Glu Phe Phe Met Val Asn Gln Leu Asn Asn Thr Arg Lys Thr			
435	440	445	
tta aag tat aat cca gtt tcc aaa gat att ata gcg agt aca aga gat			1392
Leu Lys Tyr Asn Pro Val Ser Lys Asp Ile Ile Ala Ser Thr Arg Asp			
450	455	460	
tcg gaa tta gaa tta cct cca gaa act tca gat caa cca aat tat gag			1440
Ser Glu Leu Glu Leu Pro Pro Glu Thr Ser Asp Gln Pro Asn Tyr Glu			
465	470	475	480
tca tat agc cat aga tta tgt cat atc aca agt att ccc gcg acg ggt			1488
Ser Tyr Ser His Arg Leu Cys His Ile Thr Ser Ile Pro Ala Thr Gly			
485	490	495	

aac act acc gga tta gta cct gta ttt tct tgg aca cat cga agt gca	1536
Asn Thr Thr Gly Leu Val Pro Val Phe Ser Trp Thr His Arg Ser Ala	
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gat tta aac aat aca ata tat tca gat aaa atc act caa att ccg gcc	1584
Asp Leu Asn Asn Thr Ile Tyr Ser Asp Lys Ile Thr Gln Ile Pro Ala	
515 520 525	
gtt aaa tgt tgg gat aat tta ccg ttt gtt cca gtg gta aaa gga cca	1632
Val Lys Cys Trp Asp Asn Leu Pro Phe Val Pro Val Val Lys Gly Pro	
530 535 540	
gga cat aca gga ggg gat tta tta cag tat aat aga agt act ggt tct	1680
Gly His Thr Gly Gly Asp Leu Leu Gln Tyr Asn Arg Ser Thr Gly Ser	
545 550 555 560	
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Val Gly Thr Leu Phe Leu Ala Arg Tyr Gly Leu Ala Leu Glu Lys Ala	
565 570 575	
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Gly Lys Tyr Arg Val Arg Leu Arg Tyr Ala Thr Asp Ala Asp Ile Val	
580 585 590	
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Leu His Val Asn Asp Ala Gln Ile Gln Met Pro Lys Thr Met Asn Pro	
595 600 605	
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Gly Glu Asp Leu Thr Ser Lys Thr Phe Lys Val Ala Asp Ala Ile Thr	
610 615 620	
aca tta aat tta gca aca gat agt tcg cta gca ttg aaa cat aat tta	1920
Thr Leu Asn Leu Ala Thr Asp Ser Ser Leu Ala Leu Lys His Asn Leu	
625 630 635 640	
ggg gaa gac cct aat tca aca tta tct ggt ata gtt tac gtt gac cga	1968
Gly Glu Asp Pro Asn Ser Thr Leu Ser Gly Ile Val Tyr Val Asp Arg	
645 650 655	
atc gaa ttc atc cca gta gat gag aca tat gaa gcg gaa taa	2010
Ile Glu Phe Ile Pro Val Asp Glu Thr Tyr Glu Ala Glu *	
660 665	

<210> 12
 <211> 669
 <212> PRT
 <213> Bacillus thuringiensis (truncated)

<400> 12
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 1 5 10 15
 Ser Thr Ser Val Ser Asn Asp Ser Asn Arg Tyr Pro Phe Ala Asn Glu
 20 25 30

RTA01/2138018v1

65	70	75	80	
cta tca ggt tta ggg gtc cca ttt gtt ggg ccg ata gtg agt ctt tat				288
Leu Ser Gly Leu Gly Val Pro Phe Val Gly Pro Ile Val Ser Leu Tyr				
	85	90	95	
act caa ctt att gat att ctg tgg cct tca ggg caa aag agt caa tgg				336
Thr Gln Leu Ile Asp Ile Leu Trp Pro Ser Gly Gln Lys Ser Gln Trp				
	100	105	110	
gag att ttt atg gaa caa gta gaa gaa ctc ata aat caa aaa ata gca				384
Glu Ile Phe Met Glu Gln Val Glu Glu Leu Ile Asn Gln Lys Ile Ala				
	115	120	125	
gaa tat gca agg aat aaa gcg ctt tcg gaa tta gaa gga tta ggt aat				432
Glu Tyr Ala Arg Asn Lys Ala Leu Ser Glu Leu Glu Gly Leu Gly Asn				
	130	135	140	
aat tac caa tta tat cta act gcg ctt gaa gaa tgg aaa gaa aat cca				480
Asn Tyr Gln Leu Tyr Leu Thr Ala Leu Glu Glu Trp Lys Glu Asn Pro				
	145	150	155	160
aat ggt tca aga gcc tta cga gat gtg cga aat cga ttt gaa atc ctg				528
Asn Gly Ser Arg Ala Leu Arg Asp Val Arg Asn Arg Phe Glu Ile Leu				
	165	170	175	
gat agt tta ttt acg caa tac atg cca tct ttt cga gtg aca aat ttt				576
Asp Ser Leu Phe Thr Gln Tyr Met Pro Ser Phe Arg Val Thr Asn Phe				
	180	185	190	
gaa gta cca ttc ctt aca gta tat aca cag gca gcc aac ctt cat tta				624
Glu Val Pro Phe Leu Thr Val Tyr Thr Gln Ala Ala Asn Leu His Leu				
	195	200	205	
ctg tta tta aag gac gct tca att ttt gga gaa gaa tgg gga tgg tct				672
Leu Leu Leu Lys Asp Ala Ser Ile Phe Gly Glu Glu Trp Gly Trp Ser				
	210	215	220	
aca acc act att aat aac tat tat gat cgt caa atg aaa ctt act gca				720
Thr Thr Thr Ile Asn Asn Tyr Tyr Asp Arg Gln Met Lys Leu Thr Ala				
	225	230	235	240
gaa tat tct gat cac tgt gta aag tgg tat gaa act ggt tta gca aaa				768
Glu Tyr Ser Asp His Cys Val Lys Trp Tyr Glu Thr Gly Leu Ala Lys				
	245	250	255	
tta aaa ggc acg agc gct aaa caa tgg gtc gac tat aac caa ttc cgt				816
Leu Lys Gly Thr Ser Ala Lys Gln Trp Val Asp Tyr Asn Gln Phe Arg				
	260	265	270	
aga gaa atg aca ctg acg gtt tta gat gtt gtt gca tta ttc cca aat				864
Arg Glu Met Thr Leu Thr Val Leu Asp Val Val Ala Leu Phe Pro Asn				
	275	280	285	
tat gac aca cgc acg tac cca atg gaa acg aaa gca caa cta aca agg				912
Tyr Asp Thr Arg Thr Tyr Pro Met Glu Thr Lys Ala Gln Leu Thr Arg				
	290	295	300	

gaa gta tat aca gat cca ctg ggc gcg gta aac gtg tct tca att ggt	960
Glu Val Tyr Thr Asp Pro Leu Gly Ala Val Asn Val Ser Ser Ile Gly	
305 310 315 320	
tcc tgg tat gac aaa gca cct tct ttc gga gtg ata gaa tca tcc gtt	1008
Ser Trp Tyr Asp Lys Ala Pro Ser Phe Gly Val Ile Glu Ser Ser Val	
325 330 335	
att cga cca ccc cat gta ttt gat tat ata acg gga ctc aca gtg tat	1056
Ile Arg Pro Pro His Val Phe Asp Tyr Ile Thr Gly Leu Thr Val Tyr	
340 345 350	
aca caa tca aga agc att tct tcc gct cgc tat ata aga cat tgg gct	1104
Thr Gln Ser Arg Ser Ile Ser Ser Ala Arg Tyr Ile Arg His Trp Ala	
355 360 365	
ggg cat caa ata agc tat cat cgg att ttt agt gat aat att ata aaa	1152
Gly His Gln Ile Ser Tyr His Arg Ile Phe Ser Asp Asn Ile Ile Lys	
370 375 380	
cag atg tat gga act aat caa aat cta cac agc act agt acc ttt gat	1200
Gln Met Tyr Gly Thr Asn Gln Asn Leu His Ser Thr Ser Thr Phe Asp	
385 390 395 400	
ttt acg aat tat gat att tac aag acg tta tca aaa gat gcg gtg ctc	1248
Phe Thr Asn Tyr Asp Ile Tyr Lys Thr Leu Ser Lys Asp Ala Val Leu	
405 410 415	
ctt gat att gtt ttt cct ggt tat acg tat ata ttt ttt gga atg cca	1296
Leu Asp Ile Val Phe Pro Gly Tyr Thr Tyr Ile Phe Phe Gly Met Pro	
420 425 430	
gaa gtc gag ttt ttc atg gta aac caa ttg aat aat acc aga aag acg	1344
Glu Val Glu Phe Phe Met Val Asn Gln Leu Asn Asn Thr Arg Lys Thr	
435 440 445	
tta aag tat aat ccg gtt tcc aaa gat att ata gcg ggg aca aga gat	1392
Leu Lys Tyr Asn Pro Val Ser Lys Asp Ile Ile Ala Gly Thr Arg Asp	
450 455 460	
tcg gaa tta gaa tta cct cca gaa act tca gat caa cca aat tat gag	1440
Ser Glu Leu Glu Leu Pro Pro Glu Thr Ser Asp Gln Pro Asn Tyr Glu	
465 470 475 480	
tca tat agc cat aga tta tgt cat atc aca agt att ccc gcg acg ggt	1488
Ser Tyr Ser His Arg Leu Cys His Ile Thr Ser Ile Pro Ala Thr Gly	
485 490 495	
tca act acc gga tta gta cct gta ttt tct tgg aca cat cgg agt gcc	1536
Ser Thr Thr Gly Leu Val Pro Val Phe Ser Trp Thr His Arg Ser Ala	
500 505 510	
gat ctt ata aat gca gtt cat tca gat aaa att act cag att ccg gtc	1584
Asp Leu Ile Asn Ala Val His Ser Asp Lys Ile Thr Gln Ile Pro Val	
515 520 525	

gta aag gtt tct gat ttg gct ccc tct ata aca gga ggg cca aat aat	1632
Val Lys Val Ser Asp Leu Ala Pro Ser Ile Thr Gly Gly Pro Asn Asn	
530 535 540	
acc gtt gta tcg ggt cct gga ttt aca ggg ggg ggg ata ata aaa gta	1680
Thr Val Val Ser Gly Pro Gly Phe Thr Gly Gly Gly Ile Ile Lys Val	
545 550 555 560	
ata aga aat gga gta att ata tca cat atg cgt gtt aaa att tca gac	1728
Ile Arg Asn Gly Val Ile Ile Ser His Met Arg Val Lys Ile Ser Asp	
565 570 575	
att aac aaa gaa tat agt atg agg att cgg tat gct tcc gct aat aat	1776
Ile Asn Lys Glu Tyr Ser Met Arg Ile Arg Tyr Ala Ser Ala Asn Asn	
580 585 590	
act gaa ttt tat ata aat cct tct gaa gaa aac gtt aaa tct cac gct	1824
Thr Glu Phe Tyr Ile Asn Pro Ser Glu Glu Asn Val Lys Ser His Ala	
595 600 605	
caa aaa act atg aat aga ggt gaa gct tta aca tat aat aaa ttt aat	1872
Gln Lys Thr Met Asn Arg Gly Glu Ala Leu Thr Tyr Asn Lys Phe Asn	
610 615 620	
tat gcg act ttg ccc cct att aaa ttt acg aca acc gaa cct ttc att	1920
Tyr Ala Thr Leu Pro Pro Ile Lys Phe Thr Thr Thr Glu Pro Phe Ile	
625 630 635 640	
act cta ggg gct ata ttt gaa gcg gaa gac ttt ctt gga att gaa gct	1968
Thr Leu Gly Ala Ile Phe Glu Ala Glu Asp Phe Leu Gly Ile Glu Ala	
645 650 655	
tat ata gac cga atc gaa ttt atc cca gta gat gag aca tat gaa gcg	2016
Tyr Ile Asp Arg Ile Glu Phe Ile Pro Val Asp Glu Thr Tyr Glu Ala	
660 665 670	
gaa taa	2022
Glu *	

<210> 14

<211> 673

<212> PRT

<213> Bacillus thuringiensis (truncated)

<400> 14

Met Ser Pro Asn Asn Gln Asn Glu Tyr Glu Ile Ile Asp Ala Thr Pro	
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Pro Thr Asn Ala Leu Gln Asn Met Asp Tyr Lys Asp Tyr Leu Lys Met	
35 40 45	
Ser Ala Gly Asn Ala Ser Glu Tyr Pro Gly Ser Pro Glu Val Leu Val	
50 55 60	
Ser Gly Gln Asp Ala Ala Lys Ala Ala Ile Asp Ile Val Gly Lys Leu	
65 70 75 80	

Leu Ser Gly Leu Gly Val Pro Phe Val Gly Pro Ile Val Ser Leu Tyr
 85 90 95
 Thr Gln Leu Ile Asp Ile Leu Trp Pro Ser Gly Gln Lys Ser Gln Trp
 100 105 110
 Glu Ile Phe Met Glu Gln Val Glu Glu Leu Ile Asn Gln Lys Ile Ala
 115 120 125
 Glu Tyr Ala Arg Asn Lys Ala Leu Ser Glu Leu Glu Gly Leu Gly Asn
 130 135 140
 Asn Tyr Gln Leu Tyr Leu Thr Ala Leu Glu Glu Trp Lys Glu Asn Pro
 145 150 155 160
 Asn Gly Ser Arg Ala Leu Arg Asp Val Arg Asn Arg Phe Glu Ile Leu
 165 170 175
 Asp Ser Leu Phe Thr Gln Tyr Met Pro Ser Phe Arg Val Thr Asn Phe
 180 185 190
 Glu Val Pro Phe Leu Thr Val Tyr Thr Gln Ala Ala Asn Leu His Leu
 195 200 205
 Leu Leu Leu Lys Asp Ala Ser Ile Phe Gly Glu Glu Trp Gly Trp Ser
 210 215 220
 Thr Thr Thr Ile Asn Asn Tyr Tyr Asp Arg Gln Met Lys Leu Thr Ala
 225 230 235 240
 Glu Tyr Ser Asp His Cys Val Lys Trp Tyr Glu Thr Gly Leu Ala Lys
 245 250 255
 Leu Lys Gly Thr Ser Ala Lys Gln Trp Val Asp Tyr Asn Gln Phe Arg
 260 265 270
 Arg Glu Met Thr Leu Thr Val Leu Asp Val Val Ala Leu Phe Pro Asn
 275 280 285
 Tyr Asp Thr Arg Thr Tyr Pro Met Glu Thr Lys Ala Gln Leu Thr Arg
 290 295 300
 Glu Val Tyr Thr Asp Pro Leu Gly Ala Val Asn Val Ser Ser Ile Gly
 305 310 315 320
 Ser Trp Tyr Asp Lys Ala Pro Ser Phe Gly Val Ile Glu Ser Ser Val
 325 330 335
 Ile Arg Pro Pro His Val Phe Asp Tyr Ile Thr Gly Leu Thr Val Tyr
 340 345 350
 Thr Gln Ser Arg Ser Ile Ser Ser Ala Arg Tyr Ile Arg His Trp Ala
 355 360 365
 Gly His Gln Ile Ser Tyr His Arg Ile Phe Ser Asp Asn Ile Ile Lys
 370 375 380
 Gln Met Tyr Gly Thr Asn Gln Asn Leu His Ser Thr Ser Thr Phe Asp
 385 390 395 400
 Phe Thr Asn Tyr Asp Ile Tyr Lys Thr Leu Ser Lys Asp Ala Val Leu
 405 410 415
 Leu Asp Ile Val Phe Pro Gly Tyr Thr Tyr Ile Phe Phe Gly Met Pro
 420 425 430
 Glu Val Glu Phe Phe Met Val Asn Gln Leu Asn Asn Thr Arg Lys Thr
 435 440 445
 Leu Lys Tyr Asn Pro Val Ser Lys Asp Ile Ile Ala Gly Thr Arg Asp
 450 455 460
 Ser Glu Leu Glu Leu Pro Pro Glu Thr Ser Asp Gln Pro Asn Tyr Glu
 465 470 475 480
 Ser Tyr Ser His Arg Leu Cys His Ile Thr Ser Ile Pro Ala Thr Gly
 485 490 495
 Ser Thr Thr Gly Leu Val Pro Val Phe Ser Trp Thr His Arg Ser Ala
 500 505 510
 Asp Leu Ile Asn Ala Val His Ser Asp Lys Ile Thr Gln Ile Pro Val
 515 520 525
 Val Lys Val Ser Asp Leu Ala Pro Ser Ile Thr Gly Gly Pro Asn Asn

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      530              535              540
Thr Val Val Ser Gly Pro Gly Phe Thr Gly Gly Gly Ile Ile Lys Val
545              550              555              560
Ile Arg Asn Gly Val Ile Ile Ser His Met Arg Val Lys Ile Ser Asp
      565              570              575
Ile Asn Lys Glu Tyr Ser Met Arg Ile Arg Tyr Ala Ser Ala Asn Asn
      580              585              590
Thr Glu Phe Tyr Ile Asn Pro Ser Glu Glu Asn Val Lys Ser His Ala
      595              600              605
Gln Lys Thr Met Asn Arg Gly Glu Ala Leu Thr Tyr Asn Lys Phe Asn
      610              615              620
Tyr Ala Thr Leu Pro Pro Ile Lys Phe Thr Thr Thr Glu Pro Phe Ile
625              630              635              640
Thr Leu Gly Ala Ile Phe Glu Ala Glu Asp Phe Leu Gly Ile Glu Ala
      645              650              655
Tyr Ile Asp Arg Ile Glu Phe Ile Pro Val Asp Glu Thr Tyr Glu Ala
      660              665              670
Glu

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<210> 15
<211> 1860
<212> DNA
<213> Bacillus thuringiensis (truncated)

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<220>
<221> CDS
<222> (10)...(1860)

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<221> misc_feature
<222> (0)...(0)
<223> 49PVD

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<400> 15
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      Met Ser Ala Gly Asn Ala Ser Glu Tyr Pro Gly Ser Pro Glu
              1              5              10

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gta ctt gtt agc gga caa gat gca gct aag gcc gca att gat ata gta 99
Val Leu Val Ser Gly Gln Asp Ala Ala Lys Ala Ala Ile Asp Ile Val
      15              20              25              30

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ggg aaa tta cta tca ggt tta ggg gtc cca ttt gtt ggg ccg ata gtg 147
Gly Lys Leu Leu Ser Gly Leu Gly Val Pro Phe Val Gly Pro Ile Val
              35              40              45

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agt ctt tat act caa ctt att gat att ctg tgg cct tca ggg gaa aag 195
Ser Leu Tyr Thr Gln Leu Ile Asp Ile Leu Trp Pro Ser Gly Glu Lys
              50              55              60

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agt caa tgg gaa att ttt atg gaa caa gta gaa gaa ctc att aat caa 243
Ser Gln Trp Glu Ile Phe Met Glu Gln Val Glu Glu Leu Ile Asn Gln
      65              70              75

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aaa ata gca gaa tat gca agg aat aaa gcg ctt tcg gaa tta gaa gga 291
Lys Ile Ala Glu Tyr Ala Arg Asn Lys Ala Leu Ser Glu Leu Glu Gly

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80	85	90	
tta ggt aat aat tac	caa tta tat cta act	gcg ctt gaa gaa tgg gaa	339
Leu Gly Asn Asn Tyr	Gln Leu Tyr Leu Thr	Ala Leu Glu Glu Trp Glu	
95	100	105 110	
gaa aat cca aat ggt	tca aga gcc tta cga	gat gtg cga aat cga ttt	387
Glu Asn Pro Asn Gly	Ser Arg Ala Leu Arg	Asp Val Arg Asn Arg Phe	
	115	120 125	
gaa atc ctg gat agt	tta ttt acg caa tat	atg cca tct ttt aga gtg	435
Glu Ile Leu Asp Ser	Leu Phe Thr Gln Tyr	Met Pro Ser Phe Arg Val	
	130	135 140	
aca aat ttt gaa gta	cca ttc ctt act gta	tat gca atg gca gcc aac	483
Thr Asn Phe Glu Val	Pro Phe Leu Thr Val	Tyr Ala Met Ala Ala Asn	
	145	150 155	
ctt cat tta ctg tta	tta aag gac gcg tca	att ttt gga gaa gaa tgg	531
Leu His Leu Leu Leu	Leu Lys Asp Ala Ser	Ile Phe Gly Glu Glu Trp	
	160	165 170	
gga tgg tca aca act	act att aat aac tat	tat gat cgt caa atg aaa	579
Gly Trp Ser Thr Thr	Thr Ile Asn Asn Tyr	Tyr Asp Arg Gln Met Lys	
	175	180 185 190	
ctt act gca gaa tat	tct gat cac tgt gta	aag tgg tat gaa act ggt	627
Leu Thr Ala Glu Tyr	Ser Asp His Cys Val	Lys Trp Tyr Glu Thr Gly	
	195	200 205	
tta gca aaa tta aaa	ggc acg agc gct aaa	caa tgg gtt gac tat aac	675
Leu Ala Lys Leu Lys	Gly Thr Ser Ala Lys	Gln Trp Val Asp Tyr Asn	
	210	215 220	
caa ttc cgt aga gaa	atg aca ctg gcg gtt	tta gat gtt gtt gca tta	723
Gln Phe Arg Arg Glu	Met Thr Leu Ala Val	Leu Asp Val Val Ala Leu	
	225	230 235	
ttc cca aat tat gac	aca cgc acg tac cca	atg gaa acg aaa gca caa	771
Phe Pro Asn Tyr Asp	Thr Arg Thr Tyr Pro	Met Glu Thr Lys Ala Gln	
	240	245 250	
cta aca agg gaa gta	tat aca gat cca ctg	ggc gcg gta aac gtg tct	819
Leu Thr Arg Glu Val	Thr Asp Pro Leu Gly	Ala Val Asn Val Ser	
	255	260 265 270	
tca att ggt tcc tgg	tat gac aaa gca cct	tct ttc gga gtg ata gaa	867
Ser Ile Gly Ser Trp	Tyr Asp Lys Ala Pro	Ser Phe Gly Val Ile Glu	
	275	280 285	
tca tcc gtt att cga	cca ccc cat gta ttt	gat tat ata acg gga ctc	915
Ser Ser Val Ile Arg	Pro Pro His Val Phe	Asp Tyr Ile Thr Gly Leu	
	290	295 300	
aca gtg tat aca caa	tca aga agc att tct	tcc gct cgc tat ata aga	963
Thr Val Tyr Thr Gln	Ser Arg Ser Ile Ser	Ser Ala Arg Tyr Ile Arg	
	305	310 315	

cat tgg gct ggt cat caa ata agc tac cat cgt gtc agt agg ggt agt	1011
His Trp Ala Gly His Gln Ile Ser Tyr His Arg Val Ser Arg Gly Ser	
320 325 330	
aat ctt caa caa atg tat gga act aat caa aat cta cac agc act agt	1059
Asn Leu Gln Gln Met Tyr Gly Thr Asn Gln Asn Leu His Ser Thr Ser	
335 340 345 350	
acc ttt gat ttt acg aat tat gat att tac aag act cta tca aag gat	1107
Thr Phe Asp Phe Thr Asn Tyr Asp Ile Tyr Lys Thr Leu Ser Lys Asp	
355 360 365	
gca gta ctc ctt gat att gtt tac cct ggt tat acg tat ata ttt ttt	1155
Ala Val Leu Leu Asp Ile Val Tyr Pro Gly Tyr Thr Tyr Ile Phe Phe	
370 375 380	
gga atg cca gaa gtc gag ttt ttc atg gta aac caa ttg aat aat acc	1203
Gly Met Pro Glu Val Glu Phe Phe Met Val Asn Gln Leu Asn Asn Thr	
385 390 395	
aga aag acg tta aag tat aat cca gtt tcc aaa gat att ata gcg agt	1251
Arg Lys Thr Leu Lys Tyr Asn Pro Val Ser Lys Asp Ile Ile Ala Ser	
400 405 410	
aca aga gat tcg gaa tta gaa tta cct cca gaa act tca gat caa cca	1299
Thr Arg Asp Ser Glu Leu Glu Leu Pro Pro Glu Thr Ser Asp Gln Pro	
415 420 425 430	
aat tat gag tca tat agc cat aga tta tgt cat atc aca agt att ccc	1347
Asn Tyr Glu Ser Tyr Ser His Arg Leu Cys His Ile Thr Ser Ile Pro	
435 440 445	
gcg acg ggt aac act acc gga tta gta cct gta ttt tct tgg aca cat	1395
Ala Thr Gly Asn Thr Thr Gly Leu Val Pro Val Phe Ser Trp Thr His	
450 455 460	
cga agt gca gat tta aac aat aca ata tat tca gat aaa atc act caa	1443
Arg Ser Ala Asp Leu Asn Asn Thr Ile Tyr Ser Asp Lys Ile Thr Gln	
465 470 475	
att ccg gcc gtt aaa tgt tgg gat aat tta ccg ttt gtt cca gtg gta	1491
Ile Pro Ala Val Lys Cys Trp Asp Asn Leu Pro Phe Val Pro Val Val	
480 485 490	
aaa gga cca gga cat aca gga ggg gat tta tta cag tat aat aga agt	1539
Lys Gly Pro Gly His Thr Gly Gly Asp Leu Leu Gln Tyr Asn Arg Ser	
495 500 505 510	
act ggt tct gta gga acc tta ttt cta gct cga tat ggc cta gca tta	1587
Thr Gly Ser Val Gly Thr Leu Phe Leu Ala Arg Tyr Gly Leu Ala Leu	
515 520 525	
gaa aaa gca ggg aaa tat cgt gta aga ctg aga tat gct act gat gca	1635
Glu Lys Ala Gly Lys Tyr Arg Val Arg Leu Arg Tyr Ala Thr Asp Ala	
530 535 540	

gat att gta ttg cat gta aac gat gct cag att cag atg cca aaa aca	1683
Asp Ile Val Leu His Val Asn Asp Ala Gln Ile Gln Met Pro Lys Thr	
545 550 555	
atg aac cca ggt gag gat ctg aca tct aaa act ttt aaa gtt gca gat	1731
Met Asn Pro Gly Glu Asp Leu Thr Ser Lys Thr Phe Lys Val Ala Asp	
560 565 570	
gct atc aca aca tta aat tta gca aca gat agt tcg cta gca ttg aaa	1779
Ala Ile Thr Thr Leu Asn Leu Ala Thr Asp Ser Ser Leu Ala Leu Lys	
575 580 585 590	
cat aat tta ggt gaa gac cct aat tca aca tta tct ggt ata gtt tac	1827
His Asn Leu Gly Glu Asp Pro Asn Ser Thr Leu Ser Gly Ile Val Tyr	
595 600 605	
gtt gac cga atc gaa ttc atc cca gta gat taa	1860
Val Asp Arg Ile Glu Phe Ile Pro Val Asp *	
610 615	

<210> 16
 <211> 616
 <212> PRT
 <213> *Bacillus thuringiensis* (truncated)

<400> 16

Met Ser Ala Gly Asn Ala Ser Glu Tyr Pro Gly Ser Pro Glu Val Leu	
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Val Ser Gly Gln Asp Ala Ala Lys Ala Ala Ile Asp Ile Val Gly Lys	
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35 40 45	
Tyr Thr Gln Leu Ile Asp Ile Leu Trp Pro Ser Gly Glu Lys Ser Gln	
50 55 60	
Trp Glu Ile Phe Met Glu Gln Val Glu Glu Leu Ile Asn Gln Lys Ile	
65 70 75 80	
Ala Glu Tyr Ala Arg Asn Lys Ala Leu Ser Glu Leu Glu Gly Leu Gly	
85 90 95	
Asn Asn Tyr Gln Leu Tyr Leu Thr Ala Leu Glu Glu Trp Glu Glu Asn	
100 105 110	
Pro Asn Gly Ser Arg Ala Leu Arg Asp Val Arg Asn Arg Phe Glu Ile	
115 120 125	
Leu Asp Ser Leu Phe Thr Gln Tyr Met Pro Ser Phe Arg Val Thr Asn	
130 135 140	
Phe Glu Val Pro Phe Leu Thr Val Tyr Ala Met Ala Ala Asn Leu His	
145 150 155 160	
Leu Leu Leu Leu Lys Asp Ala Ser Ile Phe Gly Glu Glu Trp Gly Trp	
165 170 175	
Ser Thr Thr Thr Ile Asn Asn Tyr Tyr Asp Arg Gln Met Lys Leu Thr	
180 185 190	
Ala Glu Tyr Ser Asp His Cys Val Lys Trp Tyr Glu Thr Gly Leu Ala	
195 200 205	
Lys Leu Lys Gly Thr Ser Ala Lys Gln Trp Val Asp Tyr Asn Gln Phe	
210 215 220	
Arg Arg Glu Met Thr Leu Ala Val Leu Asp Val Val Ala Leu Phe Pro	
225 230 235 240	

Asn	Tyr	Asp	Thr	Arg	Thr	Tyr	Pro	Met	Glu	Thr	Lys	Ala	Gln	Leu	Thr	245	250	255
Arg	Glu	Val	Tyr	Thr	Asp	Pro	Leu	Gly	Ala	Val	Asn	Val	Ser	Ser	Ile	260	265	270
Gly	Ser	Trp	Tyr	Asp	Lys	Ala	Pro	Ser	Phe	Gly	Val	Ile	Glu	Ser	Ser	275	280	285
Val	Ile	Arg	Pro	Pro	His	Val	Phe	Asp	Tyr	Ile	Thr	Gly	Leu	Thr	Val	290	295	300
Tyr	Thr	Gln	Ser	Arg	Ser	Ile	Ser	Ser	Ala	Arg	Tyr	Ile	Arg	His	Trp	305	310	315
Ala	Gly	His	Gln	Ile	Ser	Tyr	His	Arg	Val	Ser	Arg	Gly	Ser	Asn	Leu	325	330	335
Gln	Gln	Met	Tyr	Gly	Thr	Asn	Gln	Asn	Leu	His	Ser	Thr	Ser	Thr	Phe	340	345	350
Asp	Phe	Thr	Asn	Tyr	Asp	Ile	Tyr	Lys	Thr	Leu	Ser	Lys	Asp	Ala	Val	355	360	365
Leu	Leu	Asp	Ile	Val	Tyr	Pro	Gly	Tyr	Thr	Tyr	Ile	Phe	Phe	Gly	Met	370	375	380
Pro	Glu	Val	Glu	Phe	Phe	Met	Val	Asn	Gln	Leu	Asn	Asn	Thr	Arg	Lys	385	390	395
Thr	Leu	Lys	Tyr	Asn	Pro	Val	Ser	Lys	Asp	Ile	Ile	Ala	Ser	Thr	Arg	405	410	415
Asp	Ser	Glu	Leu	Glu	Leu	Pro	Pro	Glu	Thr	Ser	Asp	Gln	Pro	Asn	Tyr	420	425	430
Glu	Ser	Tyr	Ser	His	Arg	Leu	Cys	His	Ile	Thr	Ser	Ile	Pro	Ala	Thr	435	440	445
Gly	Asn	Thr	Thr	Gly	Leu	Val	Pro	Val	Phe	Ser	Trp	Thr	His	Arg	Ser	450	455	460
Ala	Asp	Leu	Asn	Asn	Thr	Ile	Tyr	Ser	Asp	Lys	Ile	Thr	Gln	Ile	Pro	465	470	475
Ala	Val	Lys	Cys	Trp	Asp	Asn	Leu	Pro	Phe	Val	Pro	Val	Val	Lys	Gly	485	490	495
Pro	Gly	His	Thr	Gly	Gly	Asp	Leu	Leu	Gln	Tyr	Asn	Arg	Ser	Thr	Gly	500	505	510
Ser	Val	Gly	Thr	Leu	Phe	Leu	Ala	Arg	Tyr	Gly	Leu	Ala	Leu	Glu	Lys	515	520	525
Ala	Gly	Lys	Tyr	Arg	Val	Arg	Leu	Arg	Tyr	Ala	Thr	Asp	Ala	Asp	Ile	530	535	540
Val	Leu	His	Val	Asn	Asp	Ala	Gln	Ile	Gln	Met	Pro	Lys	Thr	Met	Asn	545	550	555
Pro	Gly	Glu	Asp	Leu	Thr	Ser	Lys	Thr	Phe	Lys	Val	Ala	Asp	Ala	Ile	565	570	575
Thr	Thr	Leu	Asn	Leu	Ala	Thr	Asp	Ser	Ser	Leu	Ala	Leu	Lys	His	Asn	580	585	590
Leu	Gly	Glu	Asp	Pro	Asn	Ser	Thr	Leu	Ser	Gly	Ile	Val	Tyr	Val	Asp	595	600	605
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Arg Val Thr Asn Phe Glu Val Pro Phe Leu Thr Val Tyr Ala Met Ala				
145 150 155 160				
gcc aac ctt cat tta ctg tta tta aag gac gcg tca att ttt gga gaa	528			
Ala Asn Leu His Leu Leu Leu Leu Lys Asp Ala Ser Ile Phe Gly Glu				
165 170 175				
gaa tgg gga tgg tca aca act act att aat aac tat tat gat cgt caa	576			
Glu Trp Gly Trp Ser Thr Thr Thr Ile Asn Asn Tyr Tyr Asp Arg Gln				
180 185 190				
atg aaa ctt act gca gaa tat tct gat cac tgt gta aag tgg tat gaa	624			
Met Lys Leu Thr Ala Glu Tyr Ser Asp His Cys Val Lys Trp Tyr Glu				
195 200 205				
act ggt tta gca aaa tta aaa ggc acg agc gct aaa caa tgg gtt gac	672			
Thr Gly Leu Ala Lys Leu Lys Gly Thr Ser Ala Lys Gln Trp Val Asp				
210 215 220				
tat aac caa ttc cgt aga gaa atg aca ctg gcg gtt tta gat gtt gtt	720			
Tyr Asn Gln Phe Arg Arg Glu Met Thr Leu Ala Val Leu Asp Val Val				
225 230 235 240				

gca tta ttc cca aat tat gac aca cgc acg tac cca atg gaa acg aaa	768
Ala Leu Phe Pro Asn Tyr Asp Thr Arg Thr Tyr Pro Met Glu Thr Lys	
245 250 255	
gca caa cta aca agg gaa gta tat aca gat cca ctg ggc gcg gta aac	816
Ala Gln Leu Thr Arg Glu Val Tyr Thr Asp Pro Leu Gly Ala Val Asn	
260 265 270	
gtg tct tca att ggt tcc tgg tat gac aaa gca cct tct ttc gga gtg	864
Val Ser Ser Ile Gly Ser Trp Tyr Asp Lys Ala Pro Ser Phe Gly Val	
275 280 285	
ata gaa tca tcc gtt att cga cca ccc cat gta ttt gat tat ata acg	912
Ile Glu Ser Ser Val Ile Arg Pro Pro His Val Phe Asp Tyr Ile Thr	
290 295 300	
gga ctc aca gtg tat aca caa tca aga agc att tct tcc gct cgc tat	960
Gly Leu Thr Val Tyr Thr Gln Ser Arg Ser Ile Ser Ser Ala Arg Tyr	
305 310 315 320	
ata aga cat tgg gct ggt cat caa ata agc tac cat cgt gtc agt agg	1008
Ile Arg His Trp Ala Gly His Gln Ile Ser Tyr His Arg Val Ser Arg	
325 330 335	
ggt agt aat ctt caa caa atg tat gga act aat caa aat cta cac agc	1056
Gly Ser Asn Leu Gln Gln Met Tyr Gly Thr Asn Gln Asn Leu His Ser	
340 345 350	
act agt acc ttt gat ttt acg aat tat gat att tac aag act cta tca	1104
Thr Ser Thr Phe Asp Phe Thr Asn Tyr Asp Ile Tyr Lys Thr Leu Ser	
355 360 365	
aag gat gca gta ctc ctt gat att gtt tac cct ggt tat acg tat ata	1152
Lys Asp Ala Val Leu Leu Asp Ile Val Tyr Pro Gly Tyr Thr Tyr Ile	
370 375 380	
ttt ttt gga atg cca gaa gtc gag ttt ttc atg gta aac caa ttg aat	1200
Phe Phe Gly Met Pro Glu Val Glu Phe Phe Met Val Asn Gln Leu Asn	
385 390 395 400	
aat acc aga aag acg tta aag tat aat cca gtt tcc aaa gat att ata	1248
Asn Thr Arg Lys Thr Leu Lys Tyr Asn Pro Val Ser Lys Asp Ile Ile	
405 410 415	
gcg agt aca aga gat tcg gaa tta gaa tta cct cca gaa act tca gat	1296
Ala Ser Thr Arg Asp Ser Glu Leu Glu Leu Pro Pro Glu Thr Ser Asp	
420 425 430	
caa cca aat tat gag tca tat agc cat aga tta tgt cat atc aca agt	1344
Gln Pro Asn Tyr Glu Ser Tyr Ser His Arg Leu Cys His Ile Thr Ser	
435 440 445	
att ccc gcg acg ggt aac act acc gga tta gta cct gta ttt tct tgg	1392
Ile Pro Ala Thr Gly Asn Thr Thr Gly Leu Val Pro Val Phe Ser Trp	
450 455 460	

aca cat cga agt gca gat tta aac aat aca ata tat tca gat aaa atc 1440
 Thr His Arg Ser Ala Asp Leu Asn Asn Thr Ile Tyr Ser Asp Lys Ile
 465 470 475 480

act caa att ccg gcc gtt aaa tgt tgg gat aat tta ccg ttt gtt cca 1488
 Thr Gln Ile Pro Ala Val Lys Cys Trp Asp Asn Leu Pro Phe Val Pro
 485 490 495

gtg gta aaa gga cca gga cat aca gga ggg gat tta tta cag tat aat 1536
 Val Val Lys Gly Pro Gly His Thr Gly Gly Asp Leu Leu Gln Tyr Asn
 500 505 510

aga agt act ggt tct gta gga acc tta ttt cta gct cga tat ggc cta 1584
 Arg Ser Thr Gly Ser Val Gly Thr Leu Phe Leu Ala Arg Tyr Gly Leu
 515 520 525

gca tta gaa aaa gca ggg aaa tat cgt gta aga ctg aga tat gct act 1632
 Ala Leu Glu Lys Ala Gly Lys Tyr Arg Val Arg Leu Arg Tyr Ala Thr
 530 535 540

gat gca gat att gta ttg cat gta aac gat gct cag att cag atg cca 1680
 Asp Ala Asp Ile Val Leu His Val Asn Asp Ala Gln Ile Gln Met Pro
 545 550 555 560

aaa aca atg aac cca ggt gag gat ctg aca tct aaa act ttt aaa gtt 1728
 Lys Thr Met Asn Pro Gly Glu Asp Leu Thr Ser Lys Thr Phe Lys Val
 565 570 575

gca gat gct atc aca aca tta aat tta gca aca gat agt tcg cta gca 1776
 Ala Asp Ala Ile Thr Thr Leu Asn Leu Ala Thr Asp Ser Ser Leu Ala
 580 585 590

ttg aaa cat aat tta ggt gaa gac cct aat tca aca tta tct ggt ata 1824
 Leu Lys His Asn Leu Gly Glu Asp Pro Asn Ser Thr Leu Ser Gly Ile
 595 600 605

gtt tac gtt gac cga atc gaa ttc atc cca gta gat taa 1863
 Val Tyr Val Asp Arg Ile Glu Phe Ile Pro Val Asp *
 610 615 620

<210> 20

<211> 620

<212> PRT

<213> *Bacillus thuringiensis* (mutated)

<400> 20

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 Val Ser Gly Gln Asp Ala Ala Lys Ala Ala Ile Asp Ile Val Gly Lys
 20 25 30
 Leu Leu Ser Gly Leu Gly Val Pro Phe Val Gly Pro Ile Val Ser Leu
 35 40 45
 Tyr Thr Gln Leu Ile Asp Ile Leu Trp Pro Ser Gly Glu Lys Ser Gln
 50 55 60
 Trp Glu Ile Phe Met Glu Gln Val Glu Glu Leu Ile Asn Gln Lys Ile
 65 70 75 80

Ala	Glu	Tyr	Ala	Arg	Asn	Lys	Ala	Leu	Ser	Glu	Leu	Glu	Gly	Leu	Gly	85	90	95
Asn	Asn	Tyr	Gln	Leu	Tyr	Leu	Thr	Ala	Leu	Glu	Glu	Trp	Glu	Glu	Asn	100	105	110
Pro	Asn	Gly	Ser	Arg	Asn	Gly	Ser	Arg	Ala	Leu	Arg	Asp	Val	Arg	Asn	115	120	125
Arg	Phe	Glu	Ile	Leu	Asp	Ser	Leu	Phe	Thr	Gln	Tyr	Met	Pro	Ser	Phe	130	135	140
Arg	Val	Thr	Asn	Phe	Glu	Val	Pro	Phe	Leu	Thr	Val	Tyr	Ala	Met	Ala	145	150	155
Ala	Asn	Leu	His	Leu	Leu	Leu	Leu	Lys	Asp	Ala	Ser	Ile	Phe	Gly	Glu	165	170	175
Glu	Trp	Gly	Trp	Ser	Thr	Thr	Thr	Ile	Asn	Asn	Tyr	Tyr	Asp	Arg	Gln	180	185	190
Met	Lys	Leu	Thr	Ala	Glu	Tyr	Ser	Asp	His	Cys	Val	Lys	Trp	Tyr	Glu	195	200	205
Thr	Gly	Leu	Ala	Lys	Leu	Lys	Gly	Thr	Ser	Ala	Lys	Gln	Trp	Val	Asp	210	215	220
Tyr	Asn	Gln	Phe	Arg	Arg	Glu	Met	Thr	Leu	Ala	Val	Leu	Asp	Val	Val	225	230	235
Ala	Leu	Phe	Pro	Asn	Tyr	Asp	Thr	Arg	Thr	Tyr	Pro	Met	Glu	Thr	Lys	245	250	255
Ala	Gln	Leu	Thr	Arg	Glu	Val	Tyr	Thr	Asp	Pro	Leu	Gly	Ala	Val	Asn	260	265	270
Val	Ser	Ser	Ile	Gly	Ser	Trp	Tyr	Asp	Lys	Ala	Pro	Ser	Phe	Gly	Val	275	280	285
Ile	Glu	Ser	Ser	Val	Ile	Arg	Pro	Pro	His	Val	Phe	Asp	Tyr	Ile	Thr	290	295	300
Gly	Leu	Thr	Val	Tyr	Thr	Gln	Ser	Arg	Ser	Ile	Ser	Ser	Ala	Arg	Tyr	305	310	315
Ile	Arg	His	Trp	Ala	Gly	His	Gln	Ile	Ser	Tyr	His	Arg	Val	Ser	Arg	325	330	335
Gly	Ser	Asn	Leu	Gln	Gln	Met	Tyr	Gly	Thr	Asn	Gln	Asn	Leu	His	Ser	340	345	350
Thr	Ser	Thr	Phe	Asp	Phe	Thr	Asn	Tyr	Asp	Ile	Tyr	Lys	Thr	Leu	Ser	355	360	365
Lys	Asp	Ala	Val	Leu	Leu	Asp	Ile	Val	Tyr	Pro	Gly	Tyr	Thr	Tyr	Ile	370	375	380
Phe	Phe	Gly	Met	Pro	Glu	Val	Glu	Phe	Phe	Met	Val	Asn	Gln	Leu	Asn	385	390	395
Asn	Thr	Arg	Lys	Thr	Leu	Lys	Tyr	Asn	Pro	Val	Ser	Lys	Asp	Ile	Ile	405	410	415
Ala	Ser	Thr	Arg	Asp	Ser	Glu	Leu	Glu	Leu	Pro	Pro	Glu	Thr	Ser	Asp	420	425	430
Gln	Pro	Asn	Tyr	Glu	Ser	Tyr	Ser	His	Arg	Leu	Cys	His	Ile	Thr	Ser	435	440	445
Ile	Pro	Ala	Thr	Gly	Asn	Thr	Thr	Gly	Leu	Val	Pro	Val	Phe	Ser	Trp	450	455	460
Thr	His	Arg	Ser	Ala	Asp	Leu	Asn	Asn	Thr	Ile	Tyr	Ser	Asp	Lys	Ile	465	470	475
Thr	Gln	Ile	Pro	Ala	Val	Lys	Cys	Trp	Asp	Asn	Leu	Pro	Phe	Val	Pro	485	490	495
Val	Val	Lys	Gly	Pro	Gly	His	Thr	Gly	Gly	Asp	Leu	Leu	Gln	Tyr	Asn	500	505	510
Arg	Ser	Thr	Gly	Ser	Val	Gly	Thr	Leu	Phe	Leu	Ala	Arg	Tyr	Gly	Leu	515	520	525
Ala	Leu	Glu	Lys	Ala	Gly	Lys	Tyr	Arg	Val	Arg	Leu	Arg	Tyr	Ala	Thr			

530 535 540
 Asp Ala Asp Ile Val Leu His Val Asn Asp Ala Gln Ile Gln Met Pro
 545 550 555 560
 Lys Thr Met Asn Pro Gly Glu Asp Leu Thr Ser Lys Thr Phe Lys Val
 565 570 575
 Ala Asp Ala Ile Thr Thr Leu Asn Leu Ala Thr Asp Ser Ser Leu Ala
 580 585 590
 Leu Lys His Asn Leu Gly Glu Asp Pro Asn Ser Thr Leu Ser Gly Ile
 595 600 605
 Val Tyr Val Asp Arg Ile Glu Phe Ile Pro Val Asp
 610 615 620

<210> 21
 <211> 2022
 <212> DNA
 <213> *Bacillus thuringiensis* (mutated)

<220>
 <221> CDS
 <222> (1)...(2022)

<400> 21
 atg agt cca aat aat caa aat gaa tat gaa att ata gat gcg aca cct 48
 Met Ser Pro Asn Asn Gln Asn Glu Tyr Glu Ile Ile Asp Ala Thr Pro
 1 5 10 15

 tct act tct gta tcc aat gat tct aac aga tac cct ttt gcg aat gag 96
 Ser Thr Ser Val Ser Asn Asp Ser Asn Arg Tyr Pro Phe Ala Asn Glu
 20 25 30

 cca aca aat gcg cta caa aat atg gat tat aaa gat tat tta aaa atg 144
 Pro Thr Asn Ala Leu Gln Asn Met Asp Tyr Lys Asp Tyr Leu Lys Met
 35 40 45

 tct gcg gga aat gct agt gaa tac cct ggt tca cct gaa gta ctt gtt 192
 Ser Ala Gly Asn Ala Ser Glu Tyr Pro Gly Ser Pro Glu Val Leu Val
 50 55 60

 agc gga caa gat gca gct aag gcc gca att gat ata gta ggt aaa tta 240
 Ser Gly Gln Asp Ala Ala Lys Ala Ala Ile Asp Ile Val Gly Lys Leu
 65 70 75 80

 cta tca ggt tta ggg gtc cca ttt gtt ggg ccg ata gtg agt ctt tat 288
 Leu Ser Gly Leu Gly Val Pro Phe Val Gly Pro Ile Val Ser Leu Tyr
 85 90 95

 act caa ctt att gat att ctg tgg cct tca ggg gaa aag agt caa tgg 336
 Thr Gln Leu Ile Asp Ile Leu Trp Pro Ser Gly Glu Lys Ser Gln Trp
 100 105 110

 gaa att ttt atg gaa caa gta gaa gaa ctc att aat caa aaa ata gca 384
 Glu Ile Phe Met Glu Gln Val Glu Glu Leu Ile Asn Gln Lys Ile Ala
 115 120 125

 gaa tat gca agg aat aaa gcg ctt tcg gaa tta gaa gga tta ggt aat 432
 Glu Tyr Ala Arg Asn Lys Ala Leu Ser Glu Leu Glu Gly Leu Gly Asn

130	135	140	
aat tac caa tta tat cta act gcg ctt gaa gaa tgg gaa gaa aat cca			480
Asn Tyr Gln Leu Tyr Leu Thr Ala Leu Glu Glu Trp Glu Glu Asn Pro			
145	150	155	160
ttt cga cga ggt ttt cga cga ggt gcc tta cga gat gtg cga aat cga			528
Phe Arg Arg Gly Phe Arg Arg Gly Ala Leu Arg Asp Val Arg Asn Arg			
	165	170	175
ttt gaa atc ctg gat agt tta ttt acg caa tat atg cca tct ttt aga			576
Phe Glu Ile Leu Asp Ser Leu Phe Thr Gln Tyr Met Pro Ser Phe Arg			
	180	185	190
gtg aca aat ttt gaa gta cca ttc ctt act gta tat gca atg gca gcc			624
Val Thr Asn Phe Glu Val Pro Phe Leu Thr Val Tyr Ala Met Ala Ala			
	195	200	205
aac ctt cat tta ctg tta tta aag gac gcg tca att ttt gga gaa gaa			672
Asn Leu His Leu Leu Leu Lys Asp Ala Ser Ile Phe Gly Glu Glu			
	210	215	220
tgg gga tgg tca aca act act att aat aac tat tat gat cgt caa atg			720
Trp Gly Trp Ser Thr Thr Thr Ile Asn Asn Tyr Tyr Asp Arg Gln Met			
	225	230	235
aaa ctt act gca gaa tat tct gat cac tgt gta aag tgg tat gaa act			768
Lys Leu Thr Ala Glu Tyr Ser Asp His Cys Val Lys Trp Tyr Glu Thr			
	245	250	255
ggt tta gca aaa tta aaa ggc acg agc gct aaa caa tgg gtt gac tat			816
Gly Leu Ala Lys Leu Lys Gly Thr Ser Ala Lys Gln Trp Val Asp Tyr			
	260	265	270
aac caa ttc cgt aga gaa atg aca ctg gcg gtt tta gat gtt gtt gca			864
Asn Gln Phe Arg Arg Glu Met Thr Leu Ala Val Leu Asp Val Val Ala			
	275	280	285
tta ttc cca aat tat gac aca cgc acg tac cca atg gaa acg aaa gca			912
Leu Phe Pro Asn Tyr Asp Thr Arg Thr Tyr Pro Met Glu Thr Lys Ala			
	290	295	300
caa cta aca agg gaa gta tat aca gat cca ctg ggc gcg gta aac gtg			960
Gln Leu Thr Arg Glu Val Tyr Thr Asp Pro Leu Gly Ala Val Asn Val			
	305	310	315
tct tca att ggt tcc tgg tat gac aaa gca cct tct ttc gga gtg ata			1008
Ser Ser Ile Gly Ser Trp Tyr Asp Lys Ala Pro Ser Phe Gly Val Ile			
	325	330	335
gaa tca tcc gtt att cga cca ccc cat gta ttt gat tat ata acg gga			1056
Glu Ser Ser Val Ile Arg Pro Pro His Val Phe Asp Tyr Ile Thr Gly			
	340	345	350
ctc aca gtg tat aca caa tca aga agc att tct tcc gct cgc tat ata			1104
Leu Thr Val Tyr Thr Gln Ser Arg Ser Ile Ser Ser Ala Arg Tyr Ile			
	355	360	365

aga cat tgg gct ggt cat caa ata agc tac cat cgt gtc agt agg ggt	1152
Arg His Trp Ala Gly His Gln Ile Ser Tyr His Arg Val Ser Arg Gly	
370 375 380	
agt aat ctt caa caa atg tat gga act aat caa aat cta cac agc act	1200
Ser Asn Leu Gln Gln Met Tyr Gly Thr Asn Gln Asn Leu His Ser Thr	
385 390 395 400	
agt acc ttt gat ttt acg aat tat gat att tac aag act cta tca aag	1248
Ser Thr Phe Asp Phe Thr Asn Tyr Asp Ile Tyr Lys Thr Leu Ser Lys	
405 410 415	
gat gca gta ctc ctt gat att gtt tac cct ggt tat acg tat ata ttt	1296
Asp Ala Val Leu Leu Asp Ile Val Tyr Pro Gly Tyr Thr Tyr Ile Phe	
420 425 430	
ttt gga atg cca gaa gtc gag ttt ttc atg gta aac caa ttg aat aat	1344
Phe Gly Met Pro Glu Val Glu Phe Phe Met Val Asn Gln Leu Asn Asn	
435 440 445	
acc aga aag acg tta aag tat aat cca gtt tcc aaa gat att ata gcg	1392
Thr Arg Lys Thr Leu Lys Tyr Asn Pro Val Ser Lys Asp Ile Ile Ala	
450 455 460	
agt aca aga gat tcg gaa tta gaa tta cct cca gaa act tca gat caa	1440
Ser Thr Arg Asp Ser Glu Leu Glu Leu Pro Pro Glu Thr Ser Asp Gln	
465 470 475 480	
cca aat tat gag tca tat agc cat aga tta tgt cat atc aca agt att	1488
Pro Asn Tyr Glu Ser Tyr Ser His Arg Leu Cys His Ile Thr Ser Ile	
485 490 495	
ccc gcg acg ggt aac act acc gga tta gta cct gta ttt tct tgg aca	1536
Pro Ala Thr Gly Asn Thr Thr Gly Leu Val Pro Val Phe Ser Trp Thr	
500 505 510	
cat cga agt gca gat tta aac aat aca ata tat tca gat aaa atc act	1584
His Arg Ser Ala Asp Leu Asn Asn Thr Ile Tyr Ser Asp Lys Ile Thr	
515 520 525	
caa att ccg gcc gtt aaa tgt tgg gat aat tta ccg ttt gtt cca gtg	1632
Gln Ile Pro Ala Val Lys Cys Trp Asp Asn Leu Pro Phe Val Pro Val	
530 535 540	
gta aaa gga cca gga cat aca gga ggg gat tta tta cag tat aat aga	1680
Val Lys Gly Pro Gly His Thr Gly Gly Asp Leu Leu Gln Tyr Asn Arg	
545 550 555 560	
agt act ggt tct gta gga acc tta ttt cta gct cga tat ggc cta gca	1728
Ser Thr Gly Ser Val Gly Thr Leu Phe Leu Ala Arg Tyr Gly Leu Ala	
565 570 575	
tta gaa aaa gca ggg aaa tat cgt gta aga ctg aga tat gct act gat	1776
Leu Glu Lys Ala Gly Lys Tyr Arg Val Arg Leu Arg Tyr Ala Thr Asp	
580 585 590	

gca gat att gta ttg cat gta aac gat gct cag att cag atg cca aaa	1824
Ala Asp Ile Val Leu His Val Asn Asp Ala Gln Ile Gln Met Pro Lys	
595 600 605	
aca atg aac cca ggt gag gat ctg aca tct aaa act ttt aaa gtt gca	1872
Thr Met Asn Pro Gly Glu Asp Leu Thr Ser Lys Thr Phe Lys Val Ala	
610 615 620	
gat gct atc aca aca gta aat tta gca aca gat agt tcg gta gca gtg	1920
Asp Ala Ile Thr Thr Val Asn Leu Ala Thr Asp Ser Ser Val Ala Val	
625 630 635 640	
aaa cat aat gta ggt gaa gac cct aat tca aca tta tct ggt ata gtt	1968
Lys His Asn Val Gly Glu Asp Pro Asn Ser Thr Leu Ser Gly Ile Val	
645 650 655	
tac gtt gac cga atc gaa ttc atc cca gta gat gag aca tat gaa gcg	2016
Tyr Val Asp Arg Ile Glu Phe Ile Pro Val Asp Glu Thr Tyr Glu Ala	
660 665 670	
gaa taa	2022
Glu *	

<210> 22
 <211> 673
 <212> PRT
 <213> *Bacillus thuringiensis* (mutated)

<400> 22

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Ser Thr Ser Val Ser Asn Asp Ser Asn Arg Tyr Pro Phe Ala Asn Glu	
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Pro Thr Asn Ala Leu Gln Asn Met Asp Tyr Lys Asp Tyr Leu Lys Met	
35 40 45	
Ser Ala Gly Asn Ala Ser Glu Tyr Pro Gly Ser Pro Glu Val Leu Val	
50 55 60	
Ser Gly Gln Asp Ala Ala Lys Ala Ala Ile Asp Ile Val Gly Lys Leu	
65 70 75 80	
Leu Ser Gly Leu Gly Val Pro Phe Val Gly Pro Ile Val Ser Leu Tyr	
85 90 95	
Thr Gln Leu Ile Asp Ile Leu Trp Pro Ser Gly Glu Lys Ser Gln Trp	
100 105 110	
Glu Ile Phe Met Glu Gln Val Glu Glu Leu Ile Asn Gln Lys Ile Ala	
115 120 125	
Glu Tyr Ala Arg Asn Lys Ala Leu Ser Glu Leu Glu Gly Leu Gly Asn	
130 135 140	
Asn Tyr Gln Leu Tyr Leu Thr Ala Leu Glu Glu Trp Glu Glu Asn Pro	
145 150 155 160	
Phe Arg Arg Gly Phe Arg Arg Gly Ala Leu Arg Asp Val Arg Asn Arg	
165 170 175	
Phe Glu Ile Leu Asp Ser Leu Phe Thr Gln Tyr Met Pro Ser Phe Arg	
180 185 190	
Val Thr Asn Phe Glu Val Pro Phe Leu Thr Val Tyr Ala Met Ala Ala	
195 200 205	

Asn	Leu	His	Leu	Leu	Leu	Leu	Lys	Asp	Ala	Ser	Ile	Phe	Gly	Glu	Glu
210						215					220				
Trp	Gly	Trp	Ser	Thr	Thr	Thr	Ile	Asn	Asn	Tyr	Tyr	Asp	Arg	Gln	Met
225					230					235					240
Lys	Leu	Thr	Ala	Glu	Tyr	Ser	Asp	His	Cys	Val	Lys	Trp	Tyr	Glu	Thr
				245					250					255	
Gly	Leu	Ala	Lys	Leu	Lys	Gly	Thr	Ser	Ala	Lys	Gln	Trp	Val	Asp	Tyr
			260					265					270		
Asn	Gln	Phe	Arg	Arg	Glu	Met	Thr	Leu	Ala	Val	Leu	Asp	Val	Val	Ala
		275					280					285			
Leu	Phe	Pro	Asn	Tyr	Asp	Thr	Arg	Thr	Tyr	Pro	Met	Glu	Thr	Lys	Ala
	290					295					300				
Gln	Leu	Thr	Arg	Glu	Val	Tyr	Thr	Asp	Pro	Leu	Gly	Ala	Val	Asn	Val
305					310					315					320
Ser	Ser	Ile	Gly	Ser	Trp	Tyr	Asp	Lys	Ala	Pro	Ser	Phe	Gly	Val	Ile
			325						330					335	
Glu	Ser	Ser	Val	Ile	Arg	Pro	Pro	His	Val	Phe	Asp	Tyr	Ile	Thr	Gly
			340					345					350		
Leu	Thr	Val	Tyr	Thr	Gln	Ser	Arg	Ser	Ile	Ser	Ser	Ala	Arg	Tyr	Ile
	355						360					365			
Arg	His	Trp	Ala	Gly	His	Gln	Ile	Ser	Tyr	His	Arg	Val	Ser	Arg	Gly
	370					375					380				
Ser	Asn	Leu	Gln	Gln	Met	Tyr	Gly	Thr	Asn	Gln	Asn	Leu	His	Ser	Thr
385					390					395					400
Ser	Thr	Phe	Asp	Phe	Thr	Asn	Tyr	Asp	Ile	Tyr	Lys	Thr	Leu	Ser	Lys
			405						410					415	
Asp	Ala	Val	Leu	Leu	Asp	Ile	Val	Tyr	Pro	Gly	Tyr	Thr	Tyr	Ile	Phe
			420					425				430			
Phe	Gly	Met	Pro	Glu	Val	Glu	Phe	Phe	Met	Val	Asn	Gln	Leu	Asn	Asn
	435						440					445			
Thr	Arg	Lys	Thr	Leu	Lys	Tyr	Asn	Pro	Val	Ser	Lys	Asp	Ile	Ile	Ala
	450					455					460				
Ser	Thr	Arg	Asp	Ser	Glu	Leu	Glu	Leu	Pro	Pro	Glu	Thr	Ser	Asp	Gln
465					470					475					480
Pro	Asn	Tyr	Glu	Ser	Tyr	Ser	His	Arg	Leu	Cys	His	Ile	Thr	Ser	Ile
			485						490					495	
Pro	Ala	Thr	Gly	Asn	Thr	Thr	Gly	Leu	Val	Pro	Val	Phe	Ser	Trp	Thr
			500					505					510		
His	Arg	Ser	Ala	Asp	Leu	Asn	Asn	Thr	Ile	Tyr	Ser	Asp	Lys	Ile	Thr
	515						520					525			
Gln	Ile	Pro	Ala	Val	Lys	Cys	Trp	Asp	Asn	Leu	Pro	Phe	Val	Pro	Val
	530					535					540				
Val	Lys	Gly	Pro	Gly	His	Thr	Gly	Gly	Asp	Leu	Leu	Gln	Tyr	Asn	Arg
545					550					555					560
Ser	Thr	Gly	Ser	Val	Gly	Thr	Leu	Phe	Leu	Ala	Arg	Tyr	Gly	Leu	Ala
			565						570					575	
Leu	Glu	Lys	Ala	Gly	Lys	Tyr	Arg	Val	Arg	Leu	Arg	Tyr	Ala	Thr	Asp
			580					585					590		
Ala	Asp	Ile	Val	Leu	His	Val	Asn	Asp	Ala	Gln	Ile	Gln	Met	Pro	Lys
	595						600					605			
Thr	Met	Asn	Pro	Gly	Glu	Asp	Leu	Thr	Ser	Lys	Thr	Phe	Lys	Val	Ala
	610					615					620				
Asp	Ala	Ile	Thr	Thr	Val	Asn	Leu	Ala	Thr	Asp	Ser	Ser	Val	Ala	Val
625					630					635					640
Lys	His	Asn	Val	Gly	Glu	Asp	Pro	Asn	Ser	Thr	Leu	Ser	Gly	Ile	Val
			645						650					655	
Tyr	Val	Asp	Arg	Ile	Glu	Phe	Ile	Pro	Val	Asp	Glu	Thr	Tyr	Glu	Ala

Glu 660 665 670

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 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> KO forward primer

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 tttcgacgag gttttcgacg aggtgcctta cgagatgtgc gaaatcg 47

 <210> 24
 <211> 45
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> KO reverse primer

 <400> 24
 acctcgtcga aaacctcgtc gaaatggaat ttcttcccat tcttc 45

 <210> 25
 <211> 2022
 <212> DNA
 <213> *Bacillus thuringiensis* (mutated)

 <220>
 <221> CDS
 <222> (1)...(2022)

 <400> 25
 atg agt cca aat aat caa aat gaa tat gaa att ata gat gcg aca cct 48
 Met Ser Pro Asn Asn Gln Asn Glu Tyr Glu Ile Ile Asp Ala Thr Pro
 1 5 10 15

 tct act tct gta tcc aat gat tct aac aga tac cct ttt gcg aat gag 96
 Ser Thr Ser Val Ser Asn Asp Ser Asn Arg Tyr Pro Phe Ala Asn Glu
 20 25 30

 cca aca aat gcg cta caa aat atg gat tat aaa gat tat tta aaa atg 144
 Pro Thr Asn Ala Leu Gln Asn Met Asp Tyr Lys Asp Tyr Leu Lys Met
 35 40 45

 tct gcg gga aat gct agt gaa tac cct ggt tca cct gaa gta ctt gtt 192
 Ser Ala Gly Asn Ala Ser Glu Tyr Pro Gly Ser Pro Glu Val Leu Val
 50 55 60

 agc gga caa gat gca gct aag gcc gca att gat ata gta ggt aaa tta 240
 Ser Gly Gln Asp Ala Ala Lys Ala Ala Ile Asp Ile Val Gly Lys Leu
 65 70 75 80

cta tca ggt tta ggg gtc cca ttt gtt ggg ccg ata gtg agt ctt tat	288
Leu Ser Gly Leu Gly Val Pro Phe Val Gly Pro Ile Val Ser Leu Tyr	
85 90 95	
act caa ctt att gat att ctg tgg cct tca ggg gaa aag agt caa tgg	336
Thr Gln Leu Ile Asp Ile Leu Trp Pro Ser Gly Glu Lys Ser Gln Trp	
100 105 110	
gaa att ttt atg gaa caa gta gaa gaa ctc att aat caa aaa ata gca	384
Glu Ile Phe Met Glu Gln Val Glu Glu Leu Ile Asn Gln Lys Ile Ala	
115 120 125	
gaa tat gca agg aat aaa gcg ctt tcg gaa tta gaa gga tta ggt aat	432
Glu Tyr Ala Arg Asn Lys Ala Leu Ser Glu Leu Glu Gly Leu Gly Asn	
130 135 140	
aat tac caa tta tat cta act gcg ctt gaa gaa tgg gaa gaa aat cca	480
Asn Tyr Gln Leu Tyr Leu Thr Ala Leu Glu Trp Glu Glu Asn Pro	
145 150 155 160	
aat ggt tca aga aat ggt tcc cgg gcc tta cga gat gtg cga aat cga	528
Asn Gly Ser Arg Asn Gly Ser Arg Ala Leu Arg Asp Val Arg Asn Arg	
165 170 175	
ttt gaa atc ctg gat agt tta ttt acg caa tat atg cca tct ttt aga	576
Phe Glu Ile Leu Asp Ser Leu Phe Thr Gln Tyr Met Pro Ser Phe Arg	
180 185 190	
gtg aca aat ttt gaa gta cca ttc ctt act gta tat gca atg gca gcc	624
Val Thr Asn Phe Glu Val Pro Phe Leu Thr Val Tyr Ala Met Ala Ala	
195 200 205	
aac ctt cat tta ctg tta tta aag gac gcg tca att ttt gga gaa gaa	672
Asn Leu His Leu Leu Leu Leu Lys Asp Ala Ser Ile Phe Gly Glu Glu	
210 215 220	
tgg gga tgg tca aca act act att aat aac tat tat gat cgt caa atg	720
Trp Gly Trp Ser Thr Thr Thr Ile Asn Asn Tyr Tyr Asp Arg Gln Met	
225 230 235 240	
aaa ctt act gca gaa tat tct gat cac tgt gta aag tgg tat gaa act	768
Lys Leu Thr Ala Glu Tyr Ser Asp His Cys Val Lys Trp Tyr Glu Thr	
245 250 255	
ggt tta gca aaa tta aaa ggc acg agc gct aaa caa tgg gtt gac tat	816
Gly Leu Ala Lys Leu Lys Gly Thr Ser Ala Lys Gln Trp Val Asp Tyr	
260 265 270	
aac caa ttc cgt aga gaa atg aca ctg gcg gtt tta gat gtt gtt gca	864
Asn Gln Phe Arg Arg Glu Met Thr Leu Ala Val Leu Asp Val Val Ala	
275 280 285	
tta ttc cca aat tat gac aca cgc acg tac cca atg gaa acg aaa gca	912
Leu Phe Pro Asn Tyr Asp Thr Arg Thr Tyr Pro Met Glu Thr Lys Ala	
290 295 300	
caa cta aca agg gaa gta tat aca gat cca ctg ggc gcg gta aac gtg	960

Gln	Leu	Thr	Arg	Glu	Val	Tyr	Thr	Asp	Pro	Leu	Gly	Ala	Val	Asn	Val		
305					310					315					320		
tct	tca	att	ggg	tcc	tgg	tat	gac	aaa	gca	cct	tct	ttc	gga	gtg	ata	1008	
Ser	Ser	Ile	Gly	Ser	Trp	Tyr	Asp	Lys	Ala	Pro	Ser	Phe	Gly	Val	Ile		
				325					330						335		
gaa	tca	tcc	ggt	att	cga	cca	ccc	cat	gta	ttt	gat	tat	ata	acg	gga	1056	
Glu	Ser	Ser	Val	Ile	Arg	Pro	Pro	His	Val	Phe	Asp	Tyr	Ile	Thr	Gly		
			340					345						350			
ctc	aca	gtg	tat	aca	caa	tca	aga	agc	att	tct	tcc	gct	cgc	tat	ata	1104	
Leu	Thr	Val	Tyr	Thr	Gln	Ser	Arg	Ser	Ile	Ser	Ser	Ala	Arg	Tyr	Ile		
		355					360						365				
aga	cat	tgg	gct	ggg	cat	caa	ata	agc	tac	cat	cgt	gtc	agt	agg	ggg	1152	
Arg	His	Trp	Ala	Gly	His	Gln	Ile	Ser	Tyr	His	Arg	Val	Ser	Arg	Gly		
	370					375					380						
agt	aat	ctt	caa	caa	atg	tat	gga	act	aat	caa	aat	cta	cac	agc	act	1200	
Ser	Asn	Leu	Gln	Gln	Met	Tyr	Gly	Thr	Asn	Gln	Asn	Leu	His	Ser	Thr		
385					390					395					400		
agt	acc	ttt	gat	ttt	acg	aat	tat	gat	att	tac	aag	act	cta	tca	aag	1248	
Ser	Thr	Phe	Asp	Phe	Thr	Asn	Tyr	Asp	Ile	Tyr	Lys	Thr	Leu	Ser	Lys		
				405					410						415		
gat	gca	gta	ctc	ctt	gat	att	gtt	tac	cct	ggg	tat	acg	tat	ata	ttt	1296	
Asp	Ala	Val	Leu	Leu	Asp	Ile	Val	Tyr	Pro	Gly	Tyr	Thr	Tyr	Ile	Phe		
			420					425						430			
ttt	gga	atg	cca	gaa	gtc	gag	ttt	ttc	atg	gta	aac	caa	ttg	aat	aat	1344	
Phe	Gly	Met	Pro	Glu	Val	Glu	Phe	Phe	Met	Val	Asn	Gln	Leu	Asn	Asn		
	435					440						445					
acc	aga	aag	acg	tta	aag	tat	aat	cca	gtt	tcc	aaa	gat	att	ata	gcg	1392	
Thr	Arg	Lys	Thr	Leu	Lys	Tyr	Asn	Pro	Val	Ser	Lys	Asp	Ile	Ile	Ala		
	450					455					460						
agt	aca	aga	gat	tcg	gaa	tta	gaa	tta	cct	cca	gaa	act	tca	gat	caa	1440	
Ser	Thr	Arg	Asp	Ser	Glu	Leu	Glu	Leu	Pro	Pro	Glu	Thr	Ser	Asp	Gln		
465					470				475						480		
cca	aat	tat	gag	tca	tat	agc	cat	aga	tta	tgt	cat	atc	aca	agt	att	1488	
Pro	Asn	Tyr	Glu	Ser	Tyr	Ser	His	Arg	Leu	Cys	His	Ile	Thr	Ser	Ile		
			485					490						495			
ccc	gcg	acg	ggg	aac	act	acc	gga	tta	gta	cct	gta	ttt	tct	tgg	aca	1536	
Pro	Ala	Thr	Gly	Asn	Thr	Thr	Gly	Leu	Val	Pro	Val	Phe	Ser	Trp	Thr		
			500					505						510			
cat	cga	agt	gca	gat	tta	aac	aat	aca	ata	tat	tca	gat	aaa	atc	act	1584	
His	Arg	Ser	Ala	Asp	Leu	Asn	Asn	Thr	Ile	Tyr	Ser	Asp	Lys	Ile	Thr		
			515					520					525				
caa	att	ccg	gcc	gtt	aaa	tgt	tgg	gat	aat	tta	ccg	ttt	gtt	cca	gtg	1632	
Gln	Ile	Pro	Ala	Val	Lys	Cys	Trp	Asp	Asn	Leu	Pro	Phe	Val	Pro	Val		

530	535	540	
gta aaa gga cca gga cat	aca gga ggg gat	tta tta cag tat aat aga	1680
Val Lys Gly Pro Gly His Thr Gly Gly Asp	Leu Leu Gln Tyr Asn Arg		
545	550	555	560
agt act ggt tct gta gga acc tta ttt cta gct cga tat ggc cta gca			1728
Ser Thr Gly Ser Val Gly Thr Leu Phe Leu Ala Arg Tyr Gly Leu Ala			
565	570	575	
tta gaa aaa gca ggg aaa tat cgt gta aga ctg aga tat gct act gat			1776
Leu Glu Lys Ala Gly Lys Tyr Arg Val Arg Leu Arg Tyr Ala Thr Asp			
580	585	590	
gca gat att gta ttg cat gta aac gat gct cag att cag atg cca aaa			1824
Ala Asp Ile Val Leu His Val Asn Asp Ala Gln Ile Gln Met Pro Lys			
595	600	605	
aca atg aac cca ggt gag gat ctg aca tct aaa act ttt aaa gtt gca			1872
Thr Met Asn Pro Gly Glu Asp Leu Thr Ser Lys Thr Phe Lys Val Ala			
610	615	620	
gat gct atc aca aca tta aat tta gca aca gat agt tcg cta gca ttg			1920
Asp Ala Ile Thr Thr Leu Asn Leu Ala Thr Asp Ser Ser Leu Ala Leu			
625	630	635	640
aaa cat aat gta ggt gaa gac cct aat tca aca tta tct ggt ata gtt			1968
Lys His Asn Val Gly Glu Asp Pro Asn Ser Thr Leu Ser Gly Ile Val			
645	650	655	
tac gtt gac cga atc gaa ttc atc cca gta gat gag aca tat gaa gcg			2016
Tyr Val Asp Arg Ile Glu Phe Ile Pro Val Asp Glu Thr Tyr Glu Ala			
660	665	670	
gaa taa			2022
Glu *			

<210> 26
 <211> 673
 <212> PRT
 <213> Bacillus thuringiensis (mutated)

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 20 25 30
 Pro Thr Asn Ala Leu Gln Asn Met Asp Tyr Lys Asp Tyr Leu Lys Met
 35 40 45
 Ser Ala Gly Asn Ala Ser Glu Tyr Pro Gly Ser Pro Glu Val Leu Val
 50 55 60
 Ser Gly Gln Asp Ala Ala Lys Ala Ala Ile Asp Ile Val Gly Lys Leu
 65 70 75 80
 Leu Ser Gly Leu Gly Val Pro Phe Val Gly Pro Ile Val Ser Leu Tyr
 85 90 95

Thr	Gln	Leu	Ile	Asp	Ile	Leu	Trp	Pro	Ser	Gly	Glu	Lys	Ser	Gln	Trp
		100						105					110		
Glu	Ile	Phe	Met	Glu	Gln	Val	Glu	Glu	Leu	Ile	Asn	Gln	Lys	Ile	Ala
		115					120					125			
Glu	Tyr	Ala	Arg	Asn	Lys	Ala	Leu	Ser	Glu	Leu	Glu	Gly	Leu	Gly	Asn
	130					135					140				
Asn	Tyr	Gln	Leu	Tyr	Leu	Thr	Ala	Leu	Glu	Glu	Trp	Glu	Glu	Asn	Pro
145					150					155					160
Asn	Gly	Ser	Arg	Asn	Gly	Ser	Arg	Ala	Leu	Arg	Asp	Val	Arg	Asn	Arg
				165				170						175	
Phe	Glu	Ile	Leu	Asp	Ser	Leu	Phe	Thr	Gln	Tyr	Met	Pro	Ser	Phe	Arg
		180						185					190		
Val	Thr	Asn	Phe	Glu	Val	Pro	Phe	Leu	Thr	Val	Tyr	Ala	Met	Ala	Ala
	195						200					205			
Asn	Leu	His	Leu	Leu	Leu	Leu	Lys	Asp	Ala	Ser	Ile	Phe	Gly	Glu	Glu
	210					215						220			
Trp	Gly	Trp	Ser	Thr	Thr	Thr	Ile	Asn	Asn	Tyr	Tyr	Asp	Arg	Gln	Met
225					230					235					240
Lys	Leu	Thr	Ala	Glu	Tyr	Ser	Asp	His	Cys	Val	Lys	Trp	Tyr	Glu	Thr
				245					250					255	
Gly	Leu	Ala	Lys	Leu	Lys	Gly	Thr	Ser	Ala	Lys	Gln	Trp	Val	Asp	Tyr
		260						265					270		
Asn	Gln	Phe	Arg	Arg	Glu	Met	Thr	Leu	Ala	Val	Leu	Asp	Val	Val	Ala
	275						280					285			
Leu	Phe	Pro	Asn	Tyr	Asp	Thr	Arg	Thr	Tyr	Pro	Met	Glu	Thr	Lys	Ala
	290					295					300				
Gln	Leu	Thr	Arg	Glu	Val	Tyr	Thr	Asp	Pro	Leu	Gly	Ala	Val	Asn	Val
305					310					315					320
Ser	Ser	Ile	Gly	Ser	Trp	Tyr	Asp	Lys	Ala	Pro	Ser	Phe	Gly	Val	Ile
			325						330					335	
Glu	Ser	Ser	Val	Ile	Arg	Pro	Pro	His	Val	Phe	Asp	Tyr	Ile	Thr	Gly
		340						345					350		
Leu	Thr	Val	Tyr	Thr	Gln	Ser	Arg	Ser	Ile	Ser	Ser	Ala	Arg	Tyr	Ile
	355						360					365			
Arg	His	Trp	Ala	Gly	His	Gln	Ile	Ser	Tyr	His	Arg	Val	Ser	Arg	Gly
	370					375					380				
Ser	Asn	Leu	Gln	Gln	Met	Tyr	Gly	Thr	Asn	Gln	Asn	Leu	His	Ser	Thr
385					390					395					400
Ser	Thr	Phe	Asp	Phe	Thr	Asn	Tyr	Asp	Ile	Tyr	Lys	Thr	Leu	Ser	Lys
			405						410					415	
Asp	Ala	Val	Leu	Leu	Asp	Ile	Val	Tyr	Pro	Gly	Tyr	Thr	Tyr	Ile	Phe
		420						425					430		
Phe	Gly	Met	Pro	Glu	Val	Glu	Phe	Phe	Met	Val	Asn	Gln	Leu	Asn	Asn
	435						440					445			
Thr	Arg	Lys	Thr	Leu	Lys	Tyr	Asn	Pro	Val	Ser	Lys	Asp	Ile	Ile	Ala
	450					455						460			
Ser	Thr	Arg	Asp	Ser	Glu	Leu	Glu	Leu	Pro	Pro	Glu	Thr	Ser	Asp	Gln
465					470					475					480
Pro	Asn	Tyr	Glu	Ser	Tyr	Ser	His	Arg	Leu	Cys	His	Ile	Thr	Ser	Ile
			485						490					495	
Pro	Ala	Thr	Gly	Asn	Thr	Thr	Gly	Leu	Val	Pro	Val	Phe	Ser	Trp	Thr
		500						505					510		
His	Arg	Ser	Ala	Asp	Leu	Asn	Asn	Thr	Ile	Tyr	Ser	Asp	Lys	Ile	Thr
	515						520					525			
Gln	Ile	Pro	Ala	Val	Lys	Cys	Trp	Asp	Asn	Leu	Pro	Phe	Val	Pro	Val
	530					535					540				
Val	Lys	Gly	Pro	Gly	His	Thr	Gly	Gly	Asp	Leu	Leu	Gln	Tyr	Asn	Arg

20	25	30	
cca aca aat gcg cta caa aat atg gat tat aaa gat tat tta aaa atg Pro Thr Asn Ala Leu Gln Asn Met Asp Tyr Lys Asp Tyr Leu Lys Met 35 40 45			144
tct gcg gga aat gct agt gaa tac cct ggt tca cct gaa gta ctt gtt Ser Ala Gly Asn Ala Ser Glu Tyr Pro Gly Ser Pro Glu Val Leu Val 50 55 60			192
agc gga caa gat gca gct aag gcc gca att gat ata gta ggt aaa tta Ser Gly Gln Asp Ala Ala Lys Ala Ala Ile Asp Ile Val Gly Lys Leu 65 70 75 80			240
cta tca ggt tta ggg gtc cca ttt gtt ggg ccg ata gtg agt ctt tat Leu Ser Gly Leu Gly Val Pro Phe Val Gly Pro Ile Val Ser Leu Tyr 85 90 95			288
act caa ctt att gat att ctg tgg cct tca ggg gaa aag agt caa tgg Thr Gln Leu Ile Asp Ile Leu Trp Pro Ser Gly Glu Lys Ser Gln Trp 100 105 110			336
gaa att ttt atg gaa caa gta gaa gaa ctc att aat caa aaa ata gca Glu Ile Phe Met Glu Gln Val Glu Glu Leu Ile Asn Gln Lys Ile Ala 115 120 125			384
gaa tat gca agg aat aaa gcg ctt tcg gaa tta gaa gga tta ggt aat Glu Tyr Ala Arg Asn Lys Ala Leu Ser Glu Leu Glu Gly Leu Gly Asn 130 135 140			432
aat tac caa tta tat cta act gcg ctt gaa gaa tgg gaa gaa aat cca Asn Tyr Gln Leu Tyr Leu Thr Ala Leu Glu Glu Trp Glu Glu Asn Pro 145 150 155 160			480
aat ggt tca aga aat ggt tcc cgg gcc tta cga gat gtg cga aat cga Asn Gly Ser Arg Asn Gly Ser Arg Ala Leu Arg Asp Val Arg Asn Arg 165 170 175			528
ttt gaa atc ctg gat agt tta ttt acg caa tat atg cca tct ttt aga Phe Glu Ile Leu Asp Ser Leu Phe Thr Gln Tyr Met Pro Ser Phe Arg 180 185 190			576
gtg aca aat ttt gaa gta cca ttc ctt act gta tat gca atg gca gcc Val Thr Asn Phe Glu Val Pro Phe Leu Thr Val Tyr Ala Met Ala Ala 195 200 205			624
aac ctt cat tta ctg tta tta aag gac gcg tca att ttt gga gaa gaa Asn Leu His Leu Leu Leu Leu Lys Asp Ala Ser Ile Phe Gly Glu Glu 210 215 220			672
tgg gga tgg tca aca act act att aat aac tat tat gat cgt caa atg Trp Gly Trp Ser Thr Thr Thr Ile Asn Asn Tyr Tyr Asp Arg Gln Met 225 230 235 240			720
aaa ctt act gca gaa tat tct gat cac tgt gta aag tgg tat gaa act Lys Leu Thr Ala Glu Tyr Ser Asp His Cys Val Lys Trp Tyr Glu Thr 245 250 255			768

ggt tta gca aaa tta aaa ggc acg agc gct aaa caa tgg gtt gac tat	816
Gly Leu Ala Lys Leu Lys Gly Thr Ser Ala Lys Gln Trp Val Asp Tyr	
260 265 270	
aac caa ttc cgt aga gaa atg aca ctg gcg gtt tta gat gtt gtt gca	864
Asn Gln Phe Arg Arg Glu Met Thr Leu Ala Val Leu Asp Val Val Ala	
275 280 285	
tta ttc cca aat tat gac aca cgc acg tac cca atg gaa acg aaa gca	912
Leu Phe Pro Asn Tyr Asp Thr Arg Thr Tyr Pro Met Glu Thr Lys Ala	
290 295 300	
caa cta aca agg gaa gta tat aca gat cca ctg ggc gcg gta aac gtg	960
Gln Leu Thr Arg Glu Val Tyr Thr Asp Pro Leu Gly Ala Val Asn Val	
305 310 315 320	
tct tca att ggt tcc tgg tat gac aaa gca cct tct ttc gga gtg ata	1008
Ser Ser Ile Gly Ser Trp Tyr Asp Lys Ala Pro Ser Phe Gly Val Ile	
325 330 335	
gaa tca tcc gtt att cga cca ccc cat gta ttt gat tat ata acg gga	1056
Glu Ser Ser Val Ile Arg Pro Pro His Val Phe Asp Tyr Ile Thr Gly	
340 345 350	
ctc aca gtg tat aca caa tca aga agc att tct tcc gct cgc tat ata	1104
Leu Thr Val Tyr Thr Gln Ser Arg Ser Ile Ser Ser Ala Arg Tyr Ile	
355 360 365	
aga cat tgg gct ggt cat caa ata agc tac cat cgt gtc agt agg ggt	1152
Arg His Trp Ala Gly His Gln Ile Ser Tyr His Arg Val Ser Arg Gly	
370 375 380	
agt aat ctt caa caa atg tat gga act aat caa aat cta cac agc act	1200
Ser Asn Leu Gln Gln Met Tyr Gly Thr Asn Gln Asn Leu His Ser Thr	
385 390 395 400	
agt acc ttt gat ttt acg aat tat gat att tac aag act cta tca aag	1248
Ser Thr Phe Asp Phe Thr Asn Tyr Asp Ile Tyr Lys Thr Leu Ser Lys	
405 410 415	
gat gca gta ctc ctt gat att gtt tac cct ggt tat acg tat ata ttt	1296
Asp Ala Val Leu Leu Asp Ile Val Tyr Pro Gly Tyr Thr Tyr Ile Phe	
420 425 430	
ttt gga atg cca gaa gtc gag ttt ttc atg gta aac caa ttg aat aat	1344
Phe Gly Met Pro Glu Val Glu Phe Phe Met Val Asn Gln Leu Asn Asn	
435 440 445	
acc aga aag acg tta aag tat aat cca gtt tcc aaa gat att ata gcg	1392
Thr Arg Lys Thr Leu Lys Tyr Asn Pro Val Ser Lys Asp Ile Ile Ala	
450 455 460	
agt aca aga gat tcg gaa tta gaa tta cct cca gaa act tca gat caa	1440
Ser Thr Arg Asp Ser Glu Leu Glu Leu Pro Pro Glu Thr Ser Asp Gln	
465 470 475 480	

cca aat tat gag tca tat agc cat aga tta tgt cat atc aca agt att	1488
Pro Asn Tyr Glu Ser Tyr Ser His Arg Leu Cys His Ile Thr Ser Ile	
485 490 495	
ccc gcg acg ggt aac act acc gga tta gta cct gta ttt tct tgg aca	1536
Pro Ala Thr Gly Asn Thr Thr Gly Leu Val Pro Val Phe Ser Trp Thr	
500 505 510	
cat cga agt gca gat tta aac aat aca ata tat tca gat aaa atc act	1584
His Arg Ser Ala Asp Leu Asn Asn Thr Ile Tyr Ser Asp Lys Ile Thr	
515 520 525	
caa att ccg gcc gtt aaa tgt tgg gat aat tta ccg ttt gtt cca gtg	1632
Gln Ile Pro Ala Val Lys Cys Trp Asp Asn Leu Pro Phe Val Pro Val	
530 535 540	
gta aaa gga cca gga cat aca gga ggg gat tta tta cag tat aat aga	1680
Val Lys Gly Pro Gly His Thr Gly Gly Asp Leu Leu Gln Tyr Asn Arg	
545 550 555 560	
agt act ggt tct gta gga acc tta ttt cta gct cga tat ggc cta gca	1728
Ser Thr Gly Ser Val Gly Thr Leu Phe Leu Ala Arg Tyr Gly Leu Ala	
565 570 575	
tta gaa aaa gca ggg aaa tat cgt gta aga ctg aga tat gct act gat	1776
Leu Glu Lys Ala Gly Lys Tyr Arg Val Arg Leu Arg Tyr Ala Thr Asp	
580 585 590	
gca gat att gta ttg cat gta aac gat gct cag att cag atg cca aaa	1824
Ala Asp Ile Val Leu His Val Asn Asp Ala Gln Ile Gln Met Pro Lys	
595 600 605	
aca atg aac cca ggt gag gat ctg aca tct aaa act ttt aaa gtt gca	1872
Thr Met Asn Pro Gly Glu Asp Leu Thr Ser Lys Thr Phe Lys Val Ala	
610 615 620	
gat gct atc aca aca tta aat tta gca aca gat agt tcg cta gca gtg	1920
Asp Ala Ile Thr Thr Leu Asn Leu Ala Thr Asp Ser Ser Leu Ala Val	
625 630 635 640	
aaa cat aat gta ggt gaa gac cct aat tca aca tta tct ggt ata gtt	1968
Lys His Asn Val Gly Glu Asp Pro Asn Ser Thr Leu Ser Gly Ile Val	
645 650 655	
tac gtt gac cga atc gaa ttc atc cca gta gat gag aca tat gaa gcg	2016
Tyr Val Asp Arg Ile Glu Phe Ile Pro Val Asp Glu Thr Tyr Glu Ala	
660 665 670	
gaa taa	2022
Glu *	

<210> 30

<211> 673

<212> PRT

<213> Bacillus thuringiensis (mutated)

<400> 30

Met	Ser	Pro	Asn	Asn	Gln	Asn	Glu	Tyr	Glu	Ile	Ile	Asp	Ala	Thr	Pro
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Ser	Thr	Ser	Val	Ser	Asn	Asp	Ser	Asn	Arg	Tyr	Pro	Phe	Ala	Asn	Glu
			20					25					30		
Pro	Thr	Asn	Ala	Leu	Gln	Asn	Met	Asp	Tyr	Lys	Asp	Tyr	Leu	Lys	Met
		35					40					45			
Ser	Ala	Gly	Asn	Ala	Ser	Glu	Tyr	Pro	Gly	Ser	Pro	Glu	Val	Leu	Val
	50					55					60				
Ser	Gly	Gln	Asp	Ala	Ala	Lys	Ala	Ala	Ile	Asp	Ile	Val	Gly	Lys	Leu
65				70						75				80	
Leu	Ser	Gly	Leu	Gly	Val	Pro	Phe	Val	Gly	Pro	Ile	Val	Ser	Leu	Tyr
			85						90					95	
Thr	Gln	Leu	Ile	Asp	Ile	Leu	Trp	Pro	Ser	Gly	Glu	Lys	Ser	Gln	Trp
		100						105					110		
Glu	Ile	Phe	Met	Glu	Gln	Val	Glu	Glu	Leu	Ile	Asn	Gln	Lys	Ile	Ala
		115					120						125		
Glu	Tyr	Ala	Arg	Asn	Lys	Ala	Leu	Ser	Glu	Leu	Glu	Gly	Leu	Gly	Asn
	130					135					140				
Asn	Tyr	Gln	Leu	Tyr	Leu	Thr	Ala	Leu	Glu	Glu	Trp	Glu	Glu	Asn	Pro
145					150					155					160
Asn	Gly	Ser	Arg	Asn	Gly	Ser	Arg	Ala	Leu	Arg	Asp	Val	Arg	Asn	Arg
			165						170					175	
Phe	Glu	Ile	Leu	Asp	Ser	Leu	Phe	Thr	Gln	Tyr	Met	Pro	Ser	Phe	Arg
			180					185					190		
Val	Thr	Asn	Phe	Glu	Val	Pro	Phe	Leu	Thr	Val	Tyr	Ala	Met	Ala	Ala
		195					200					205			
Asn	Leu	His	Leu	Leu	Leu	Leu	Lys	Asp	Ala	Ser	Ile	Phe	Gly	Glu	Glu
	210					215					220				
Trp	Gly	Trp	Ser	Thr	Thr	Thr	Ile	Asn	Asn	Tyr	Tyr	Asp	Arg	Gln	Met
225					230					235					240
Lys	Leu	Thr	Ala	Glu	Tyr	Ser	Asp	His	Cys	Val	Lys	Trp	Tyr	Glu	Thr
			245						250					255	
Gly	Leu	Ala	Lys	Leu	Lys	Gly	Thr	Ser	Ala	Lys	Gln	Trp	Val	Asp	Tyr
			260				265						270		
Asn	Gln	Phe	Arg	Arg	Glu	Met	Thr	Leu	Ala	Val	Leu	Asp	Val	Val	Ala
		275				280						285			
Leu	Phe	Pro	Asn	Tyr	Asp	Thr	Arg	Thr	Tyr	Pro	Met	Glu	Thr	Lys	Ala
	290					295					300				
Gln	Leu	Thr	Arg	Glu	Val	Tyr	Thr	Asp	Pro	Leu	Gly	Ala	Val	Asn	Val
305					310					315					320
Ser	Ser	Ile	Gly	Ser	Trp	Tyr	Asp	Lys	Ala	Pro	Ser	Phe	Gly	Val	Ile
			325						330					335	
Glu	Ser	Ser	Val	Ile	Arg	Pro	Pro	His	Val	Phe	Asp	Tyr	Ile	Thr	Gly
			340					345					350		
Leu	Thr	Val	Tyr	Thr	Gln	Ser	Arg	Ser	Ile	Ser	Ser	Ala	Arg	Tyr	Ile
		355					360					365			
Arg	His	Trp	Ala	Gly	His	Gln	Ile	Ser	Tyr	His	Arg	Val	Ser	Arg	Gly
	370					375					380				
Ser	Asn	Leu	Gln	Gln	Met	Tyr	Gly	Thr	Asn	Gln	Asn	Leu	His	Ser	Thr
385					390					395					400
Ser	Thr	Phe	Asp	Phe	Thr	Asn	Tyr	Asp	Ile	Tyr	Lys	Thr	Leu	Ser	Lys
			405						410					415	
Asp	Ala	Val	Leu	Leu	Asp	Ile	Val	Tyr	Pro	Gly	Tyr	Thr	Tyr	Ile	Phe
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Phe	Gly	Met	Pro	Glu	Val	Glu	Phe	Phe	Met	Val	Asn	Gln	Leu	Asn	Asn

<212> DNA

<213> *Bacillus thuringiensis* (mutated)

<220>

<221> CDS

<222> (1)...(2022)

<400> 33

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tct act tct gta tcc aat gat tct aac aga tac cct ttt gcg aat gag	96
Ser Thr Ser Val Ser Asn Asp Ser Asn Arg Tyr Pro Phe Ala Asn Glu	
20 25 30	
cca aca aat gcg cta caa aat atg gat tat aaa gat tat tta aaa atg	144
Pro Thr Asn Ala Leu Gln Asn Met Asp Tyr Lys Asp Tyr Leu Lys Met	
35 40 45	
tct gcg gga aat gct agt gaa tac cct ggt tca cct gaa gta ctt gtt	192
Ser Ala Gly Asn Ala Ser Glu Tyr Pro Gly Ser Pro Glu Val Leu Val	
50 55 60	
agc gga caa gat gca gct aag gcc gca att gat ata gta ggt aaa tta	240
Ser Gly Gln Asp Ala Ala Lys Ala Ala Ile Asp Ile Val Gly Lys Leu	
65 70 75 80	
cta tca ggt tta ggg gtc cca ttt gtt ggg ccg ata gtg agt ctt tat	288
Leu Ser Gly Leu Gly Val Pro Phe Val Gly Pro Ile Val Ser Leu Tyr	
85 90 95	
act caa ctt att gat att ctg tgg cct tca ggg gaa aag agt caa tgg	336
Thr Gln Leu Ile Asp Ile Leu Trp Pro Ser Gly Glu Lys Ser Gln Trp	
100 105 110	
gaa att ttt atg gaa caa gta gaa gaa ctc att aat caa aaa ata gca	384
Glu Ile Phe Met Glu Gln Val Glu Glu Leu Ile Asn Gln Lys Ile Ala	
115 120 125	
gaa tat gca agg aat aaa gcg ctt tcg gaa tta gaa gga tta ggt aat	432
Glu Tyr Ala Arg Asn Lys Ala Leu Ser Glu Leu Glu Gly Leu Gly Asn	
130 135 140	
aat tac caa tta tat cta act gcg ctt gaa gaa tgg gaa gaa aat cca	480
Asn Tyr Gln Leu Tyr Leu Thr Ala Leu Glu Glu Trp Glu Glu Asn Pro	
145 150 155 160	
aat ggt tca aga aat ggt tcc cgg gcc tta cga gat gtg cga aat cga	528
Asn Gly Ser Arg Asn Gly Ser Arg Ala Leu Arg Asp Val Arg Asn Arg	
165 170 175	
ttt gaa atc ctg gat agt tta ttt acg caa tat atg cca tct ttt aga	576
Phe Glu Ile Leu Asp Ser Leu Phe Thr Gln Tyr Met Pro Ser Phe Arg	
180 185 190	
gtg aca aat ttt gaa gta cca ttc ctt act gta tat gca atg gca gcc	624

Val	Thr	Asn	Phe	Glu	Val	Pro	Phe	Leu	Thr	Val	Tyr	Ala	Met	Ala	Ala		
		195					200					205					
aac	ctt	cat	tta	ctg	tta	tta	aag	gac	gcg	tca	att	ttt	gga	gaa	gaa	672	
Asn	Leu	His	Leu	Leu	Leu	Leu	Lys	Asp	Ala	Ser	Ile	Phe	Gly	Glu	Glu		
	210					215					220						
tgg	gga	tgg	tca	aca	act	act	att	aat	aac	tat	tat	gat	cgt	caa	atg	720	
Trp	Gly	Trp	Ser	Thr	Thr	Thr	Ile	Asn	Asn	Tyr	Tyr	Asp	Arg	Gln	Met		
225					230					235					240		
aaa	ctt	act	gca	gaa	tat	tct	gat	cac	tgt	gta	aag	tgg	tat	gaa	act	768	
Lys	Leu	Thr	Ala	Glu	Tyr	Ser	Asp	His	Cys	Val	Lys	Trp	Tyr	Glu	Thr		
			245					250						255			
ggc	tta	gca	aaa	tta	aaa	ggc	acg	agc	gct	aaa	caa	tgg	gtt	gac	tat	816	
Gly	Leu	Ala	Lys	Leu	Lys	Gly	Thr	Ser	Ala	Lys	Gln	Trp	Val	Asp	Tyr		
			260					265					270				
aac	caa	ttc	cgt	aga	gaa	atg	aca	ctg	gcg	gtt	tta	gat	gtt	gtt	gca	864	
Asn	Gln	Phe	Arg	Arg	Glu	Met	Thr	Leu	Ala	Val	Leu	Asp	Val	Val	Ala		
		275					280					285					
tta	ttc	cca	aat	tat	gac	aca	cgc	acg	tac	cca	atg	gaa	acg	aaa	gca	912	
Leu	Phe	Pro	Asn	Tyr	Asp	Thr	Arg	Thr	Tyr	Pro	Met	Glu	Thr	Lys	Ala		
	290					295					300						
caa	cta	aca	agg	gaa	gta	tat	aca	gat	cca	ctg	ggc	gcg	gta	aac	gtg	960	
Gln	Leu	Thr	Arg	Glu	Val	Tyr	Thr	Asp	Pro	Leu	Gly	Ala	Val	Asn	Val		
305					310					315					320		
tct	tca	att	ggc	tcc	tgg	tat	gac	aaa	gca	cct	tct	ttc	gga	gtg	ata	1008	
Ser	Ser	Ile	Gly	Ser	Trp	Tyr	Asp	Lys	Ala	Pro	Ser	Phe	Gly	Val	Ile		
				325					330					335			
gaa	tca	tcc	gtt	att	cga	cca	ccc	cat	gta	ttt	gat	tat	ata	acg	gga	1056	
Glu	Ser	Ser	Val	Ile	Arg	Pro	Pro	His	Val	Phe	Asp	Tyr	Ile	Thr	Gly		
			340					345					350				
ctc	aca	gtg	tat	aca	caa	tca	aga	agc	att	tct	tcc	gct	cgc	tat	ata	1104	
Leu	Thr	Val	Tyr	Thr	Gln	Ser	Arg	Ser	Ile	Ser	Ser	Ala	Arg	Tyr	Ile		
		355					360					365					
aga	cat	tgg	gct	ggc	cat	caa	ata	agc	tac	cat	cgt	gtc	agt	agg	ggc	1152	
Arg	His	Trp	Ala	Gly	His	Gln	Ile	Ser	Tyr	His	Arg	Val	Ser	Arg	Gly		
	370					375					380						
agt	aat	ctt	caa	caa	atg	tat	gga	act	aat	caa	aat	cta	cac	agc	act	1200	
Ser	Asn	Leu	Gln	Gln	Met	Tyr	Gly	Thr	Asn	Gln	Asn	Leu	His	Ser	Thr		
385					390					395					400		
agt	acc	ttt	gat	ttt	acg	aat	tat	gat	att	tac	aag	act	cta	tca	aag	1248	
Ser	Thr	Phe	Asp	Phe	Thr	Asn	Tyr	Asp	Ile	Tyr	Lys	Thr	Leu	Ser	Lys		
				405					410					415			
gat	gca	gta	ctc	ctt	gat	att	gtt	tac	cct	ggc	tat	acg	tat	ata	ttt	1296	
Asp	Ala	Val	Leu	Leu	Asp	Ile	Val	Tyr	Pro	Gly	Tyr	Thr	Tyr	Ile	Phe		

420						425						430						
ttt gga atg cca gaa gtc gag ttt ttc atg gta aac caa ttg aat aat	1344																	
Phe Gly Met Pro Glu Val Glu Phe Phe Met Val Asn Gln Leu Asn Asn																		
435 440 445																		
acc aga aag acg tta aag tat aat cca gtt tcc aaa gat att ata gcg	1392																	
Thr Arg Lys Thr Leu Lys Tyr Asn Pro Val Ser Lys Asp Ile Ile Ala																		
450 455 460																		
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Ser Thr Arg Asp Ser Glu Leu Glu Leu Pro Pro Glu Thr Ser Asp Gln																		
465 470 475 480																		
cca aat tat gag tca tat agc cat aga tta tgt cat atc aca agt att	1488																	
Pro Asn Tyr Glu Ser Tyr Ser His Arg Leu Cys His Ile Thr Ser Ile																		
485 490 495																		
ccc gcg acg ggt aac act acc gga tta gta cct gta ttt tct tgg aca	1536																	
Pro Ala Thr Gly Asn Thr Thr Gly Leu Val Pro Val Phe Ser Trp Thr																		
500 505 510																		
cat cga agt gca gat tta aac aat aca ata tat tca gat aaa atc act	1584																	
His Arg Ser Ala Asp Leu Asn Asn Thr Ile Tyr Ser Asp Lys Ile Thr																		
515 520 525																		
caa att ccg gcc gtt aaa tgt tgg gat aat tta ccg ttt gtt cca gtg	1632																	
Gln Ile Pro Ala Val Lys Cys Trp Asp Asn Leu Pro Phe Val Pro Val																		
530 535 540																		
gta aaa gga cca gga cat aca gga ggg gat tta tta cag tat aat aga	1680																	
Val Lys Gly Pro Gly His Thr Gly Gly Asp Leu Leu Gln Tyr Asn Arg																		
545 550 555 560																		
agt act ggt tct gta gga acc tta ttt cta gct cga tat ggc cta gca	1728																	
Ser Thr Gly Ser Val Gly Thr Leu Phe Leu Ala Arg Tyr Gly Leu Ala																		
565 570 575																		
tta gaa aaa gca ggg aaa tat cgt gta aga ctg aga tat gct act gat	1776																	
Leu Glu Lys Ala Gly Lys Tyr Arg Val Arg Leu Arg Tyr Ala Thr Asp																		
580 585 590																		
gca gat att gta ttg cat gta aac gat gct cag att cag atg cca aaa	1824																	
Ala Asp Ile Val Leu His Val Asn Asp Ala Gln Ile Gln Met Pro Lys																		
595 600 605																		
aca atg aac cca ggt gag gat ctg aca tct aaa act ttt aaa gtt gca	1872																	
Thr Met Asn Pro Gly Glu Asp Leu Thr Ser Lys Thr Phe Lys Val Ala																		
610 615 620																		
gat gct atc aca aca gta aat tta gca aca gat agt tcg gta gca gtg	1920																	
Asp Ala Ile Thr Thr Val Asn Leu Ala Thr Asp Ser Ser Val Ala Val																		
625 630 635 640																		
aaa cat aat gta ggt gaa gac cct aat tca aca tta tct ggt ata gtt	1968																	
Lys His Asn Val Gly Glu Asp Pro Asn Ser Thr Leu Ser Gly Ile Val																		
645 650 655																		

tac gtt gac cga atc gaa ttc atc cca gta gat gag aca tat gaa gcg	2016
Tyr Val Asp Arg Ile Glu Phe Ile Pro Val Asp Glu Thr Tyr Glu Ala	
660 665 670	

gaa taa	2022
Glu *	

<210> 34
 <211> 673
 <212> PRT
 <213> *Bacillus thuringiensis* (mutated)

<400> 34

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Pro Thr Asn Ala Leu Gln Asn Met Asp Tyr Lys Asp Tyr Leu Lys Met	
35 40 45	
Ser Ala Gly Asn Ala Ser Glu Tyr Pro Gly Ser Pro Glu Val Leu Val	
50 55 60	
Ser Gly Gln Asp Ala Ala Lys Ala Ala Ile Asp Ile Val Gly Lys Leu	
65 70 75 80	
Leu Ser Gly Leu Gly Val Pro Phe Val Gly Pro Ile Val Ser Leu Tyr	
85 90 95	
Thr Gln Leu Ile Asp Ile Leu Trp Pro Ser Gly Glu Lys Ser Gln Trp	
100 105 110	
Glu Ile Phe Met Glu Gln Val Glu Glu Leu Ile Asn Gln Lys Ile Ala	
115 120 125	
Glu Tyr Ala Arg Asn Lys Ala Leu Ser Glu Leu Glu Gly Leu Gly Asn	
130 135 140	
Asn Tyr Gln Leu Tyr Leu Thr Ala Leu Glu Glu Trp Glu Glu Asn Pro	
145 150 155 160	
Asn Gly Ser Arg Asn Gly Ser Arg Ala Leu Arg Asp Val Arg Asn Arg	
165 170 175	
Phe Glu Ile Leu Asp Ser Leu Phe Thr Gln Tyr Met Pro Ser Phe Arg	
180 185 190	
Val Thr Asn Phe Glu Val Pro Phe Leu Thr Val Tyr Ala Met Ala Ala	
195 200 205	
Asn Leu His Leu Leu Leu Leu Lys Asp Ala Ser Ile Phe Gly Glu Glu	
210 215 220	
Trp Gly Trp Ser Thr Thr Thr Ile Asn Asn Tyr Tyr Asp Arg Gln Met	
225 230 235 240	
Lys Leu Thr Ala Glu Tyr Ser Asp His Cys Val Lys Trp Tyr Glu Thr	
245 250 255	
Gly Leu Ala Lys Leu Lys Gly Thr Ser Ala Lys Gln Trp Val Asp Tyr	
260 265 270	
Asn Gln Phe Arg Arg Glu Met Thr Leu Ala Val Leu Asp Val Val Ala	
275 280 285	
Leu Phe Pro Asn Tyr Asp Thr Arg Thr Tyr Pro Met Glu Thr Lys Ala	
290 295 300	
Gln Leu Thr Arg Glu Val Tyr Thr Asp Pro Leu Gly Ala Val Asn Val	
305 310 315 320	
Ser Ser Ile Gly Ser Trp Tyr Asp Lys Ala Pro Ser Phe Gly Val Ile	


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<210> 36
<211> 54
<212> DNA
<213> Artificial Sequence

<220>
<223> M6 reverse primer

<400> 36
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<210> 37
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> pET28 forward primer

<400> 37
taatacgact cactataggg      20

<210> 38
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> pET28 reverse primer

<400> 38
gctagttatt gctcagcgg      19

<210> 39
<211> 2028
<212> DNA
<213> Bacillus thuringiensis (mutated)

<220>
<221> CDS
<222> (1)...(2028)

<400> 39
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Met Ser Pro Asn Asn Gln Asn Glu Tyr Glu Ile Ile Asp Ala Thr Pro
1          5          10          15

tct act tct gta tcc aat gat tct aac aga tac cct ttt gcg aat gag      96
Ser Thr Ser Val Ser Asn Asp Ser Asn Arg Tyr Pro Phe Ala Asn Glu
20          25          30

cca aca aat gcg cta caa aat atg gat tat aaa gat tat tta aaa atg      144
Pro Thr Asn Ala Leu Gln Asn Met Asp Tyr Lys Asp Tyr Leu Lys Met
35          40          45

tct gcg gga aat gct agt gaa tac cct ggt tca cct gaa gta ctt gtt      192

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Ser	Ala	Gly	Asn	Ala	Ser	Glu	Tyr	Pro	Gly	Ser	Pro	Glu	Val	Leu	Val		
50						55					60						
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Ser	Gly	Gln	Asp	Ala	Ala	Lys	Ala	Ala	Ile	Asp	Ile	Val	Gly	Lys	Leu		
65					70				75						80		
cta	tca	ggg	tta	ggg	gtc	cca	ttt	gtt	ggg	ccg	ata	gtg	agt	ctt	tat	288	
Leu	Ser	Gly	Leu	Gly	Val	Pro	Phe	Val	Gly	Pro	Ile	Val	Ser	Leu	Tyr		
				85					90						95		
act	caa	ctt	att	gat	att	ctg	tgg	cct	tca	ggg	gaa	aag	agt	caa	tgg	336	
Thr	Gln	Leu	Ile	Asp	Ile	Leu	Trp	Pro	Ser	Gly	Glu	Lys	Ser	Gln	Trp		
			100					105						110			
gaa	att	ttt	atg	gaa	caa	gta	gaa	gaa	ctc	att	aat	caa	aaa	ata	gca	384	
Glu	Ile	Phe	Met	Glu	Gln	Val	Glu	Glu	Leu	Ile	Asn	Gln	Lys	Ile	Ala		
		115					120					125					
gaa	tat	gca	agg	aat	aaa	gcg	ctt	tcg	gaa	tta	gaa	gga	tta	ggg	aat	432	
Glu	Tyr	Ala	Arg	Asn	Lys	Ala	Leu	Ser	Glu	Leu	Glu	Gly	Leu	Gly	Asn		
	130					135					140						
aat	tac	caa	tta	tat	cta	act	gcg	ctt	gaa	gaa	tgg	gaa	gaa	aat	cca	480	
Asn	Tyr	Gln	Leu	Tyr	Leu	Thr	Ala	Leu	Glu	Glu	Trp	Glu	Glu	Asn	Pro		
145					150				155						160		
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Phe	Arg	Ser	Arg	Gly	Phe	Arg	Ser	Arg	Gly	Pro	Ala	Leu	Arg	Asp	Val		
				165					170						175		
cga	aat	cga	ttt	gaa	atc	ctg	gat	agt	tta	ttt	acg	caa	tat	atg	cca	576	
Arg	Asn	Arg	Phe	Glu	Ile	Leu	Asp	Ser	Leu	Phe	Thr	Gln	Tyr	Met	Pro		
			180					185						190			
tct	ttt	aga	gtg	aca	aat	ttt	gaa	gta	cca	ttc	ctt	act	gta	tat	gca	624	
Ser	Phe	Arg	Val	Thr	Asn	Phe	Glu	Val	Pro	Phe	Leu	Thr	Val	Tyr	Ala		
		195					200					205					
atg	gca	gcc	aac	ctt	cat	tta	ctg	tta	tta	aag	gac	gcg	tca	att	ttt	672	
Met	Ala	Ala	Asn	Leu	His	Leu	Leu	Leu	Leu	Lys	Asp	Ala	Ser	Ile	Phe		
		210				215					220						
gga	gaa	gaa	tgg	gga	tgg	tca	aca	act	act	att	aat	aac	tat	tat	gat	720	
Gly	Glu	Glu	Trp	Gly	Trp	Ser	Thr	Thr	Thr	Ile	Asn	Asn	Tyr	Tyr	Asp		
225					230					235					240		
cgt	caa	atg	aaa	ctt	act	gca	gaa	tat	tct	gat	cac	tgt	gta	aag	tgg	768	
Arg	Gln	Met	Lys	Leu	Thr	Ala	Glu	Tyr	Ser	Asp	His	Cys	Val	Lys	Trp		
				245					250						255		
tat	gaa	act	ggg	tta	gca	aaa	tta	aaa	ggc	acg	agc	gct	aaa	caa	tgg	816	
Tyr	Glu	Thr	Gly	Leu	Ala	Lys	Leu	Lys	Gly	Thr	Ser	Ala	Lys	Gln	Trp		
			260					265					270				
gtt	gac	tat	aac	caa	ttc	cgt	aga	gaa	atg	aca	ctg	gcg	gtt	tta	gat	864	
Val	Asp	Tyr	Asn	Gln	Phe	Arg	Arg	Glu	Met	Thr	Leu	Ala	Val	Leu	Asp		

275	280	285	
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acg aaa gca caa cta aca agg gaa gta tat aca gat cca ctg ggc gcg Thr Lys Ala Gln Leu Thr Arg Glu Val Tyr Thr Asp Pro Leu Gly Ala 305 310 315 320			960
gta aac gtg tct tca att ggt tcc tgg tat gac aaa gca cct tct ttc Val Asn Val Ser Ser Ile Gly Ser Trp Tyr Asp Lys Ala Pro Ser Phe 325 330 335			1008
gga gtg ata gaa tca tcc gtt att cga cca ccc cat gta ttt gat tat Gly Val Ile Glu Ser Ser Val Ile Arg Pro Pro His Val Phe Asp Tyr 340 345 350			1056
ata acg gga ctc aca gtg tat aca caa tca aga agc att tct tcc gct Ile Thr Gly Leu Thr Val Tyr Thr Gln Ser Arg Ser Ile Ser Ser Ala 355 360 365			1104
cgc tat ata aga cat tgg gct ggt cat caa ata agc tac cat cgt gtc Arg Tyr Ile Arg His Trp Ala Gly His Gln Ile Ser Tyr His Arg Val 370 375 380			1152
agt agg ggt agt aat ctt caa caa atg tat gga act aat caa aat cta Ser Arg Gly Ser Asn Leu Gln Gln Met Tyr Gly Thr Asn Gln Asn Leu 385 390 395 400			1200
cac agc act agt acc ttt gat ttt acg aat tat gat att tac aag act His Ser Thr Ser Thr Phe Asp Phe Thr Asn Tyr Asp Ile Tyr Lys Thr 405 410 415			1248
cta tca aag gat gca gta ctc ctt gat att gtt tac cct ggt tat acg Leu Ser Lys Asp Ala Val Leu Leu Asp Ile Val Tyr Pro Gly Tyr Thr 420 425 430			1296
tat ata ttt ttt gga atg cca gaa gtc gag ttt ttc atg gta aac caa Tyr Ile Phe Phe Gly Met Pro Glu Val Glu Phe Phe Met Val Asn Gln 435 440 445			1344
ttg aat aat acc aga aag acg tta aag tat aat cca gtt tcc aaa gat Leu Asn Asn Thr Arg Lys Thr Leu Lys Tyr Asn Pro Val Ser Lys Asp 450 455 460			1392
att ata gcg agt aca aga gat tcg gaa tta gaa tta cct cca gaa act Ile Ile Ala Ser Thr Arg Asp Ser Glu Leu Glu Leu Pro Pro Glu Thr 465 470 475 480			1440
tca gat caa cca aat tat gag tca tat agc cat aga tta tgt cat atc Ser Asp Gln Pro Asn Tyr Glu Ser Tyr Ser His Arg Leu Cys His Ile 485 490 495			1488
aca agt att ccc gcg acg ggt aac act acc gga tta gta cct gta ttt Thr Ser Ile Pro Ala Thr Gly Asn Thr Thr Gly Leu Val Pro Val Phe 500 505 510			1536

tct tgg aca cat cga agt gca gat tta aac aat aca ata tat tca gat	1584
Ser Trp Thr His Arg Ser Ala Asp Leu Asn Asn Thr Ile Tyr Ser Asp	
515 520 525	
aaa atc act caa att ccg gcc gtt aaa tgt tgg gat aat tta ccg ttt	1632
Lys Ile Thr Gln Ile Pro Ala Val Lys Cys Trp Asp Asn Leu Pro Phe	
530 535 540	
gtt cca gtg gta aaa gga cca gga cat aca gga ggg gat tta tta cag	1680
Val Pro Val Val Lys Gly Pro Gly His Thr Gly Gly Asp Leu Leu Gln	
545 550 555 560	
tat aat aga agt act ggt tct gta gga acc tta ttt cta gct cga tat	1728
Tyr Asn Arg Ser Thr Gly Ser Val Gly Thr Leu Phe Leu Ala Arg Tyr	
565 570 575	
ggc cta gca tta gaa aaa gca ggg aaa tat cgt gta aga ctg aga tat	1776
Gly Leu Ala Leu Glu Lys Ala Gly Lys Tyr Arg Val Arg Leu Arg Tyr	
580 585 590	
gct act gat gca gat att gta ttg cat gta aac gat gct cag att cag	1824
Ala Thr Asp Ala Asp Ile Val Leu His Val Asn Asp Ala Gln Ile Gln	
595 600 605	
atg cca aaa aca atg aac cca ggt gag gat ctg aca tct aaa act ttt	1872
Met Pro Lys Thr Met Asn Pro Gly Glu Asp Leu Thr Ser Lys Thr Phe	
610 615 620	
aaa gtt gca gat gct atc aca aca gtt aat tta gca aca gat agt tcg	1920
Lys Val Ala Asp Ala Ile Thr Thr Val Asn Leu Ala Thr Asp Ser Ser	
625 630 635 640	
gtt gca gtt aaa cat aat gta ggt gaa gac cct aat tca aca tta tct	1968
Val Ala Val Lys His Asn Val Gly Glu Asp Pro Asn Ser Thr Leu Ser	
645 650 655	
ggg ata gtt tac gtt gac cga atc gaa ttc atc cca gta gat gag aca	2016
Gly Ile Val Tyr Val Asp Arg Ile Glu Phe Ile Pro Val Asp Glu Thr	
660 665 670	
tat gaa gcg gaa	2028
Tyr Glu Ala Glu	
675	

<210> 40
 <211> 676
 <212> PRT
 <213> Bacillus thuringiensis (mutated)

<400> 40
 Met Ser Pro Asn Asn Gln Asn Glu Tyr Glu Ile Ile Asp Ala Thr Pro
 1 5 10 15
 Ser Thr Ser Val Ser Asn Asp Ser Asn Arg Tyr Pro Phe Ala Asn Glu
 20 25 30
 Pro Thr Asn Ala Leu Gln Asn Met Asp Tyr Lys Asp Tyr Leu Lys Met

RTA01/2138018v1

Thr Ser Ile Pro Ala Thr Gly Asn Thr Thr Gly Leu Val Pro Val Phe
 500 505 510
 Ser Trp Thr His Arg Ser Ala Asp Leu Asn Asn Thr Ile Tyr Ser Asp
 515 520 525
 Lys Ile Thr Gln Ile Pro Ala Val Lys Cys Trp Asp Asn Leu Pro Phe
 530 535 540
 Val Pro Val Val Lys Gly Pro Gly His Thr Gly Gly Asp Leu Leu Gln
 545 550 555 560
 Tyr Asn Arg Ser Thr Gly Ser Val Gly Thr Leu Phe Leu Ala Arg Tyr
 565 570 575
 Gly Leu Ala Leu Glu Lys Ala Gly Lys Tyr Arg Val Arg Leu Arg Tyr
 580 585 590
 Ala Thr Asp Ala Asp Ile Val Leu His Val Asn Asp Ala Gln Ile Gln
 595 600 605
 Met Pro Lys Thr Met Asn Pro Gly Glu Asp Leu Thr Ser Lys Thr Phe
 610 615 620
 Lys Val Ala Asp Ala Ile Thr Thr Val Asn Leu Ala Thr Asp Ser Ser
 625 630 635 640
 Val Ala Val Lys His Asn Val Gly Glu Asp Pro Asn Ser Thr Leu Ser
 645 650 655
 Gly Ile Val Tyr Val Asp Arg Ile Glu Phe Ile Pro Val Asp Glu Thr
 660 665 670
 Tyr Glu Ala Glu
 675

<210> 41
 <211> 2025
 <212> DNA
 <213> *Bacillus thuringiensis* (mutated)

<220>
 <221> CDS
 <222> (1) ... (2025)

<400> 41
 atg agt cca aat aat caa aat gaa tat gaa att ata gat gcg aca cct 48
 Met Ser Pro Asn Asn Gln Asn Glu Tyr Glu Ile Ile Asp Ala Thr Pro
 1 5 10 15
 tct act tct gta tcc aat gat tct aac aga tac cct ttt gcg aat gag 96
 Ser Thr Ser Val Ser Asn Asp Ser Asn Arg Tyr Pro Phe Ala Asn Glu
 20 25 30
 cca aca aat gcg cta caa aat atg gat tat aaa gat tat tta aaa atg 144
 Pro Thr Asn Ala Leu Gln Asn Met Asp Tyr Lys Asp Tyr Leu Lys Met
 35 40 45
 tct gcg gga aat gct agt gaa tac cct ggt tca cct gaa gta ctt gtt 192
 Ser Ala Gly Asn Ala Ser Glu Tyr Pro Gly Ser Pro Glu Val Leu Val
 50 55 60
 agc gga caa gat gca gct aag gcc gca att gat ata gta ggt aaa tta 240
 Ser Gly Gln Asp Ala Ala Lys Ala Ala Ile Asp Ile Val Gly Lys Leu
 65 70 75 80
 cta tca ggt tta ggg gtc cca ttt gtt ggg ccg ata gtg agt ctt tat 288

Leu	Ser	Gly	Leu	Gly	Val	Pro	Phe	Val	Gly	Pro	Ile	Val	Ser	Leu	Tyr	
				85					90					95		
act	caa	ctt	att	gat	att	ctg	tgg	cct	tca	ggg	gaa	aag	agt	caa	tgg	336
Thr	Gln	Leu	Ile	Asp	Ile	Leu	Trp	Pro	Ser	Gly	Glu	Lys	Ser	Gln	Trp	
			100					105					110			
gaa	att	ttt	atg	gaa	caa	gta	gaa	gaa	ctc	att	aat	caa	aaa	ata	gca	384
Glu	Ile	Phe	Met	Glu	Gln	Val	Glu	Glu	Leu	Ile	Asn	Gln	Lys	Ile	Ala	
			115				120					125				
gaa	tat	gca	agg	aat	aaa	gcg	ctt	tcg	gaa	tta	gaa	gga	tta	ggg	aat	432
Glu	Tyr	Ala	Arg	Asn	Lys	Ala	Leu	Ser	Glu	Leu	Glu	Gly	Leu	Gly	Asn	
			130				135					140				
aat	tac	caa	tta	tat	cta	act	gcg	ctt	gaa	gaa	tgg	gaa	gaa	aat	cca	480
Asn	Tyr	Gln	Leu	Tyr	Leu	Thr	Ala	Leu	Glu	Glu	Trp	Glu	Glu	Asn	Pro	
					150						155				160	
ttt	cga	agt	cga	ggg	ttt	cga	agt	cga	ggg	gcc	tta	cga	gat	gtg	cga	528
Phe	Arg	Ser	Arg	Gly	Phe	Arg	Ser	Arg	Gly	Ala	Leu	Arg	Asp	Val	Arg	
				165					170					175		
aat	cga	ttt	gaa	atc	ctg	gat	agt	tta	ttt	acg	caa	tat	atg	cca	tct	576
Asn	Arg	Phe	Glu	Ile	Leu	Asp	Ser	Leu	Phe	Thr	Gln	Tyr	Met	Pro	Ser	
				180				185					190			
ttt	aga	gtg	aca	aat	ttt	gaa	gta	cca	ttc	ctt	act	gta	tat	gca	atg	624
Phe	Arg	Val	Thr	Asn	Phe	Glu	Val	Pro	Phe	Leu	Thr	Val	Tyr	Ala	Met	
			195				200					205				
gca	gcc	aac	ctt	cat	tta	ctg	tta	tta	aag	gac	gcg	tca	att	ttt	gga	672
Ala	Ala	Asn	Leu	His	Leu	Leu	Leu	Leu	Lys	Asp	Ala	Ser	Ile	Phe	Gly	
			210				215				220					
gaa	gaa	tgg	gga	tgg	tca	aca	act	act	att	aat	aac	tat	tat	gat	cgt	720
Glu	Glu	Trp	Gly	Trp	Ser	Thr	Thr	Thr	Ile	Asn	Asn	Tyr	Tyr	Asp	Arg	
			225			230				235				240		
caa	atg	aaa	ctt	act	gca	gaa	tat	tct	gat	cac	tgt	gta	aag	tgg	tat	768
Gln	Met	Lys	Leu	Thr	Ala	Glu	Tyr	Ser	Asp	His	Cys	Val	Lys	Trp	Tyr	
				245					250					255		
gaa	act	ggg	tta	gca	aaa	tta	aaa	ggc	acg	agc	gct	aaa	caa	tgg	gtt	816
Glu	Thr	Gly	Leu	Ala	Lys	Leu	Lys	Gly	Thr	Ser	Ala	Lys	Gln	Trp	Val	
			260					265					270			
gac	tat	aac	caa	ttc	cgt	aga	gaa	atg	aca	ctg	gcg	gtt	tta	gat	gtt	864
Asp	Tyr	Asn	Gln	Phe	Arg	Arg	Glu	Met	Thr	Leu	Ala	Val	Leu	Asp	Val	
			275				280					285				
gtt	gca	tta	ttc	cca	aat	tat	gac	aca	cgc	acg	tac	cca	atg	gaa	acg	912
Val	Ala	Leu	Phe	Pro	Asn	Tyr	Asp	Thr	Arg	Thr	Tyr	Pro	Met	Glu	Thr	
			290				295				300					
aaa	gca	caa	cta	aca	agg	gaa	gta	tat	aca	gat	cca	ctg	ggc	gcg	gta	960
Lys	Ala	Gln	Leu	Thr	Arg	Glu	Val	Tyr	Thr	Asp	Pro	Leu	Gly	Ala	Val	

305	310	315	320	
aac gtg tct tca att ggt tcc tgg tat gac aaa gca cct tct ttc gga	1008			
Asn Val Ser Ser Ile Gly Ser Trp Tyr Asp Lys Ala Pro Ser Phe Gly				
325	330	335		
gtg ata gaa tca tcc gtt att cga cca ccc cat gta ttt gat tat ata	1056			
Val Ile Glu Ser Ser Val Ile Arg Pro Pro His Val Phe Asp Tyr Ile				
340	345	350		
acg gga ctc aca gtg tat aca caa tca aga agc att tct tcc gct cgc	1104			
Thr Gly Leu Thr Val Tyr Thr Gln Ser Arg Ser Ile Ser Ser Ala Arg				
355	360	365		
tat ata aga cat tgg gct ggt cat caa ata agc tac cat cgt gtc agt	1152			
Tyr Ile Arg His Trp Ala Gly His Gln Ile Ser Tyr His Arg Val Ser				
370	375	380		
agg ggt agt aat ctt caa caa atg tat gga act aat caa aat cta cac	1200			
Arg Gly Ser Asn Leu Gln Gln Met Tyr Gly Thr Asn Gln Asn Leu His				
385	390	395	400	
agc act agt acc ttt gat ttt acg aat tat gat att tac aag act cta	1248			
Ser Thr Ser Thr Phe Asp Phe Thr Asn Tyr Asp Ile Tyr Lys Thr Leu				
405	410	415		
tca aag gat gca gta ctc ctt gat att gtt tac cct ggt tat acg tat	1296			
Ser Lys Asp Ala Val Leu Leu Asp Ile Val Tyr Pro Gly Tyr Thr Tyr				
420	425	430		
ata ttt ttt gga atg cca gaa gtc gag ttt ttc atg gta aac caa ttg	1344			
Ile Phe Phe Gly Met Pro Glu Val Glu Phe Phe Met Val Asn Gln Leu				
435	440	445		
aat aat acc aga aag acg tta aag tat aat cca gtt tcc aaa gat att	1392			
Asn Asn Thr Arg Lys Thr Leu Lys Tyr Asn Pro Val Ser Lys Asp Ile				
450	455	460		
ata gcg agt aca aga gat tcg gaa tta gaa tta cct cca gaa act tca	1440			
Ile Ala Ser Thr Arg Asp Ser Glu Leu Glu Leu Pro Pro Glu Thr Ser				
465	470	475	480	
gat caa cca aat tat gag tca tat agc cat aga tta tgt cat atc aca	1488			
Asp Gln Pro Asn Tyr Glu Ser Tyr Ser His Arg Leu Cys His Ile Thr				
485	490	495		
agt att ccc gcg acg ggt aac act acc gga tta gta cct gta ttt tct	1536			
Ser Ile Pro Ala Thr Gly Asn Thr Thr Gly Leu Val Pro Val Phe Ser				
500	505	510		
tgg aca cat cga agt gca gat tta aac aat aca ata tat tca gat aaa	1584			
Trp Thr His Arg Ser Ala Asp Leu Asn Asn Thr Ile Tyr Ser Asp Lys				
515	520	525		
atc act caa att ccg gcc gtt aaa tgt tgg gat aat tta ccg ttt gtt	1632			
Ile Thr Gln Ile Pro Ala Val Lys Cys Trp Asp Asn Leu Pro Phe Val				
530	535	540		

cca gtg gta aaa gga cca gga cat aca gga ggg gat tta tta cag tat	1680
Pro Val Val Lys Gly Pro Gly His Thr Gly Gly Asp Leu Leu Gln Tyr	
545 550 555 560	
aat aga agt act ggt tct gta gga acc tta ttt cta gct cga tat ggc	1728
Asn Arg Ser Thr Gly Ser Val Gly Thr Leu Phe Leu Ala Arg Tyr Gly	
565 570 575	
cta gca tta gaa aaa gca ggg aaa tat cgt gta aga ctg aga tat gct	1776
Leu Ala Leu Glu Lys Ala Gly Lys Tyr Arg Val Arg Leu Arg Tyr Ala	
580 585 590	
act gat gca gat att gta ttg cat gta aac gat gct cag att cag atg	1824
Thr Asp Ala Asp Ile Val Leu His Val Asn Asp Ala Gln Ile Gln Met	
595 600 605	
cca aaa aca atg aac cca ggt gag gat ctg aca tct aaa act ttt aaa	1872
Pro Lys Thr Met Asn Pro Gly Glu Asp Leu Thr Ser Lys Thr Phe Lys	
610 615 620	
gtt gca gat gct atc aca aca gtt aat tta gca aca gat agt tcg gtt	1920
Val Ala Asp Ala Ile Thr Thr Val Asn Leu Ala Thr Asp Ser Ser Val	
625 630 635 640	
gca gtt aaa cat aat gta ggt gaa gac cct aat tca aca tta tct ggt	1968
Ala Val Lys His Asn Val Gly Glu Asp Pro Asn Ser Thr Leu Ser Gly	
645 650 655	
ata gtt tac gtt gac cga atc gaa ttc atc cca gta gat gag aca tat	2016
Ile Val Tyr Val Asp Arg Ile Glu Phe Ile Pro Val Asp Glu Thr Tyr	
660 665 670	
gaa gcg gaa	2025
Glu Ala Glu	
675	

<210> 42

<211> 675

<212> PRT

<213> Bacillus thuringiensis (mutated)

<400> 42

Met Ser Pro Asn Asn Gln Asn Glu Tyr Glu Ile Ile Asp Ala Thr Pro	
1 5 10 15	
Ser Thr Ser Val Ser Asn Asp Ser Asn Arg Tyr Pro Phe Ala Asn Glu	
20 25 30	
Pro Thr Asn Ala Leu Gln Asn Met Asp Tyr Lys Asp Tyr Leu Lys Met	
35 40 45	
Ser Ala Gly Asn Ala Ser Glu Tyr Pro Gly Ser Pro Glu Val Leu Val	
50 55 60	
Ser Gly Gln Asp Ala Ala Lys Ala Ala Ile Asp Ile Val Gly Lys Leu	
65 70 75 80	
Leu Ser Gly Leu Gly Val Pro Phe Val Gly Pro Ile Val Ser Leu Tyr	
85 90 95	
Thr Gln Leu Ile Asp Ile Leu Trp Pro Ser Gly Glu Lys Ser Gln Trp	

Asn	Arg	Ser	Thr	Gly	Ser	Val	Gly	Thr	Leu	Phe	Leu	Ala	Arg	Tyr	Gly	
				565					570						575	
Leu	Ala	Leu	Glu	Lys	Ala	Gly	Lys	Tyr	Arg	Val	Arg	Leu	Arg	Tyr	Ala	
			580					585						590		
Thr	Asp	Ala	Asp	Ile	Val	Leu	His	Val	Asn	Asp	Ala	Gln	Ile	Gln	Met	
		595					600					605				
Pro	Lys	Thr	Met	Asn	Pro	Gly	Glu	Asp	Leu	Thr	Ser	Lys	Thr	Phe	Lys	
	610					615					620					
Val	Ala	Asp	Ala	Ile	Thr	Thr	Val	Asn	Leu	Ala	Thr	Asp	Ser	Ser	Val	
	625				630					635					640	
Ala	Val	Lys	His	Asn	Val	Gly	Glu	Asp	Pro	Asn	Ser	Thr	Leu	Ser	Gly	
			645					650						655		
Ile	Val	Tyr	Val	Asp	Arg	Ile	Glu	Phe	Ile	Pro	Val	Asp	Glu	Thr	Tyr	
			660					665					670			
Glu	Ala	Glu														
		675														

<210> 43
 <211> 2022
 <212> DNA
 <213> Bacillus thuringiensis (mutated)

<220>
 <221> CDS
 <222> (1)...(2022)

<400> 43																
atg	agt	cca	aat	aat	caa	aat	gaa	tat	gaa	att	ata	gat	gcg	aca	cct	48
Met	Ser	Pro	Asn	Asn	Gln	Asn	Glu	Tyr	Glu	Ile	Ile	Asp	Ala	Thr	Pro	
1				5					10					15		
tct	act	tct	gta	tcc	aat	gat	tct	aac	aga	tac	cct	ttt	gcg	aat	gag	96
Ser	Thr	Ser	Val	Ser	Asn	Asp	Ser	Asn	Arg	Tyr	Pro	Phe	Ala	Asn	Glu	
			20					25					30			
cca	aca	aat	gcg	cta	caa	aat	atg	gat	tat	aaa	gat	tat	tta	aaa	atg	144
Pro	Thr	Asn	Ala	Leu	Gln	Asn	Met	Asp	Tyr	Lys	Asp	Tyr	Leu	Lys	Met	
		35					40					45				
tct	gcg	gga	aat	gct	agt	gaa	tac	cct	ggg	tca	cct	gaa	gta	ctt	gtt	192
Ser	Ala	Gly	Asn	Ala	Ser	Glu	Tyr	Pro	Gly	Ser	Pro	Glu	Val	Leu	Val	
	50					55					60					
agc	gga	caa	gat	gca	gct	aag	gcc	gca	att	gat	ata	gta	ggg	aaa	tta	240
Ser	Gly	Gln	Asp	Ala	Ala	Lys	Ala	Ala	Ile	Asp	Ile	Val	Gly	Lys	Leu	
	65				70				75						80	
cta	tca	ggg	tta	ggg	gtc	cca	ttt	gtt	ggg	ccg	ata	gtg	agt	ctt	tat	288
Leu	Ser	Gly	Leu	Gly	Val	Pro	Phe	Val	Gly	Pro	Ile	Val	Ser	Leu	Tyr	
			85					90						95		
act	caa	ctt	att	gat	att	ctg	tgg	cct	tca	ggg	gaa	aag	agt	caa	tgg	336
Thr	Gln	Leu	Ile	Asp	Ile	Leu	Trp	Pro	Ser	Gly	Glu	Lys	Ser	Gln	Trp	
			100					105					110			
gaa	att	ttt	atg	gaa	caa	gta	gaa	gaa	ctc	att	aat	caa	aaa	ata	gca	384

Glu Ile Phe Met Glu Gln Val	Glu Glu Leu Ile Asn Gln Lys Ile Ala	
115	120	125
gaa tat gca agg aat aaa gcg ctt tcg gaa tta gaa gga tta ggt aat	432	
Glu Tyr Ala Arg Asn Lys Ala Leu Ser Glu Leu Glu Gly Leu Gly Asn		
130	135	140
aat tac caa tta tat cta act gcg ctt gaa gaa tgg gaa gaa aat cca	480	
Asn Tyr Gln Leu Tyr Leu Thr Ala Leu Glu Glu Trp Glu Glu Asn Pro		
145	150	155
aat ggt tcc cgg ttt cga agt cga ggt gcc tta cga gat gtg cga aat	528	
Asn Gly Ser Arg Phe Arg Ser Arg Gly Ala Leu Arg Asp Val Arg Asn		
	165	170
cga ttt gaa atc ctg gat agt tta ttt acg caa tat atg cca tct ttt	576	
Arg Phe Glu Ile Leu Asp Ser Leu Phe Thr Gln Tyr Met Pro Ser Phe		
	180	190
aga gtg aca aat ttt gaa gta cca ttc ctt act gta tat gca atg gca	624	
Arg Val Thr Asn Phe Glu Val Pro Phe Leu Thr Val Tyr Ala Met Ala		
	195	200
gcc aac ctt cat tta ctg tta tta aag gac gcg tca att ttt gga gaa	672	
Ala Asn Leu His Leu Leu Leu Leu Lys Asp Ala Ser Ile Phe Gly Glu		
	210	220
gaa tgg gga tgg tca aca act act att aat aac tat tat gat cgt caa	720	
Glu Trp Gly Trp Ser Thr Thr Thr Ile Asn Asn Tyr Tyr Asp Arg Gln		
	225	235
atg aaa ctt act gca gaa tat tct gat cac tgt gta aag tgg tat gaa	768	
Met Lys Leu Thr Ala Glu Tyr Ser Asp His Cys Val Lys Trp Tyr Glu		
	245	250
act ggt tta gca aaa tta aaa ggc acg agc gct aaa caa tgg gtt gac	816	
Thr Gly Leu Ala Lys Leu Lys Gly Thr Ser Ala Lys Gln Trp Val Asp		
	260	270
tat aac caa ttc cgt aga gaa atg aca ctg gcg gtt tta gat gtt gtt	864	
Tyr Asn Gln Phe Arg Arg Glu Met Thr Leu Ala Val Leu Asp Val Val		
	275	285
gca tta ttc cca aat tat gac aca cgc acg tac cca atg gaa acg aaa	912	
Ala Leu Phe Pro Asn Tyr Asp Thr Arg Thr Tyr Pro Met Glu Thr Lys		
	290	300
gca caa cta aca agg gaa gta tat aca gat cca ctg ggc gcg gta aac	960	
Ala Gln Leu Thr Arg Glu Val Tyr Thr Asp Pro Leu Gly Ala Val Asn		
	305	315
gtg tct tca att ggt tcc tgg tat gac aaa gca cct tct ttc gga gtg	1008	
Val Ser Ser Ile Gly Ser Trp Tyr Asp Lys Ala Pro Ser Phe Gly Val		
	325	335
ata gaa tca tcc gtt att cga cca ccc cat gta ttt gat tat ata acg	1056	
Ile Glu Ser Ser Val Ile Arg Pro Pro His Val Phe Asp Tyr Ile Thr		

340										345										350										
gga ctc aca gtg tat aca caa tca aga agc att tct tcc gct cgc tat	1104																													
Gly Leu Thr Val Tyr Thr Gln Ser Arg Ser Ile Ser Ser Ala Arg Tyr																														
355 360 365																														
ata aga cat tgg gct ggt cat caa ata agc tac cat cgt gtc agt agg	1152																													
Ile Arg His Trp Ala Gly His Gln Ile Ser Tyr His Arg Val Ser Arg																														
370 375 380																														
ggt agt aat ctt caa caa atg tat gga act aat caa aat cta cac agc	1200																													
Gly Ser Asn Leu Gln Gln Met Tyr Gly Thr Asn Gln Asn Leu His Ser																														
385 390 395 400																														
act agt acc ttt gat ttt acg aat tat gat att tac aag act cta tca	1248																													
Thr Ser Thr Phe Asp Phe Thr Asn Tyr Asp Ile Tyr Lys Thr Leu Ser																														
405 410 415																														
aag gat gca gta ctc ctt gat att gtt tac cct ggt tat acg tat ata	1296																													
Lys Asp Ala Val Leu Leu Asp Ile Val Tyr Pro Gly Tyr Thr Tyr Ile																														
420 425 430																														
ttt ttt gga atg cca gaa gtc gag ttt ttc atg gta aac caa ttg aat	1344																													
Phe Phe Gly Met Pro Glu Val Glu Phe Phe Met Val Asn Gln Leu Asn																														
435 440 445																														
aat acc aga aag acg tta aag tat aat cca gtt tcc aaa gat att ata	1392																													
Asn Thr Arg Lys Thr Leu Lys Tyr Asn Pro Val Ser Lys Asp Ile Ile																														
450 455 460																														
gcg agt aca aga gat tcg gaa tta gaa tta cct cca gaa act tca gat	1440																													
Ala Ser Thr Arg Asp Ser Glu Leu Glu Leu Pro Pro Glu Thr Ser Asp																														
465 470 475 480																														
caa cca aat tat gag tca tat agc cat aga tta tgt cat atc aca agt	1488																													
Gln Pro Asn Tyr Glu Ser Tyr Ser His Arg Leu Cys His Ile Thr Ser																														
485 490 495																														
att ccc gcg acg ggt aac act acc gga tta gta cct gta ttt tct tgg	1536																													
Ile Pro Ala Thr Gly Asn Thr Thr Gly Leu Val Pro Val Phe Ser Trp																														
500 505 510																														
aca cat cga agt gca gat tta aac aat aca ata tat tca gat aaa atc	1584																													
Thr His Arg Ser Ala Asp Leu Asn Asn Thr Ile Tyr Ser Asp Lys Ile																														
515 520 525																														
act caa att ccg gcc gtt aaa tgt tgg gat aat tta ccg ttt gtt cca	1632																													
Thr Gln Ile Pro Ala Val Lys Cys Trp Asp Asn Leu Pro Phe Val Pro																														
530 535 540																														
gtg gta aaa gga cca gga cat aca gga ggg gat tta tta cag tat aat	1680																													
Val Val Lys Gly Pro Gly His Thr Gly Gly Asp Leu Leu Gln Tyr Asn																														
545 550 555 560																														
aga agt act ggt tct gta gga acc tta ttt cta gct cga tat ggc cta	1728																													
Arg Ser Thr Gly Ser Val Gly Thr Leu Phe Leu Ala Arg Tyr Gly Leu																														
565 570 575																														

gca tta gaa aaa gca ggg aaa tat cgt gta aga ctg aga tat gct act	1776
Ala Leu Glu Lys Ala Gly Lys Tyr Arg Val Arg Leu Arg Tyr Ala Thr	
580 585 590	
gat gca gat att gta ttg cat gta aac gat gct cag att cag atg cca	1824
Asp Ala Asp Ile Val Leu His Val Asn Asp Ala Gln Ile Gln Met Pro	
595 600 605	
aaa aca atg aac cca ggt gag gat ctg aca tct aaa act ttt aaa gtt	1872
Lys Thr Met Asn Pro Gly Glu Asp Leu Thr Ser Lys Thr Phe Lys Val	
610 615 620	
gca gat gct atc aca aca gtt aat tta gca aca gat agt tcg gtt gca	1920
Ala Asp Ala Ile Thr Val Asn Leu Ala Thr Asp Ser Ser Val Ala	
625 630 635 640	
gtt aaa cat aat gta ggt gaa gac cct aat tca aca tta tct ggt ata	1968
Val Lys His Asn Val Thr Gly Glu Asp Pro Asn Ser Thr Leu Ser Gly Ile	
645 650 655	
gtt tac gtt gac cga atc gaa ttc atc cca gta gat gag aca tat gaa	2016
Val Tyr Val Asp Arg Ile Glu Phe Ile Pro Val Asp Glu Thr Tyr Glu	
660 665 670	
gcg gaa	2022
Ala Glu	

<210> 44

<211> 674

<212> PRT

<213> Bacillus thuringiensis (mutated)

<400> 44

Met Ser Pro Asn Asn Gln Asn Glu Tyr Glu Ile Ile Asp Ala Thr Pro	
1 5 10 15	
Ser Thr Ser Val Ser Asn Asp Ser Asn Arg Tyr Pro Phe Ala Asn Glu	
20 25 30	
Pro Thr Asn Ala Leu Gln Asn Met Asp Tyr Lys Asp Tyr Leu Lys Met	
35 40 45	
Ser Ala Gly Asn Ala Ser Glu Tyr Pro Gly Ser Pro Glu Val Leu Val	
50 55 60	
Ser Gly Gln Asp Ala Ala Lys Ala Ala Ile Asp Ile Val Gly Lys Leu	
65 70 75 80	
Leu Ser Gly Leu Gly Val Pro Phe Val Gly Pro Ile Val Ser Leu Tyr	
85 90 95	
Thr Gln Leu Ile Asp Ile Leu Trp Pro Ser Gly Glu Lys Ser Gln Trp	
100 105 110	
Glu Ile Phe Met Glu Gln Val Glu Glu Leu Ile Asn Gln Lys Ile Ala	
115 120 125	
Glu Tyr Ala Arg Asn Lys Ala Leu Ser Glu Leu Glu Gly Leu Gly Asn	
130 135 140	
Asn Tyr Gln Leu Tyr Leu Thr Ala Leu Glu Glu Trp Glu Glu Asn Pro	
145 150 155 160	
Asn Gly Ser Arg Phe Arg Ser Arg Gly Ala Leu Arg Asp Val Arg Asn	

					165										175
Arg	Phe	Glu	Ile	Leu	Asp	Ser	Leu	Phe	Thr	Gln	Tyr	Met	Pro	Ser	Phe
			180					185					190		
Arg	Val	Thr	Asn	Phe	Glu	Val	Pro	Phe	Leu	Thr	Val	Tyr	Ala	Met	Ala
			195				200					205			
Ala	Asn	Leu	His	Leu	Leu	Leu	Leu	Lys	Asp	Ala	Ser	Ile	Phe	Gly	Glu
			210			215					220				
Glu	Trp	Gly	Trp	Ser	Thr	Thr	Thr	Ile	Asn	Asn	Tyr	Tyr	Asp	Arg	Gln
225				230					235					240	
Met	Lys	Leu	Thr	Ala	Glu	Tyr	Ser	Asp	His	Cys	Val	Lys	Trp	Tyr	Glu
				245				250					255		
Thr	Gly	Leu	Ala	Lys	Leu	Lys	Gly	Thr	Ser	Ala	Lys	Gln	Trp	Val	Asp
			260					265					270		
Tyr	Asn	Gln	Phe	Arg	Arg	Glu	Met	Thr	Leu	Ala	Val	Leu	Asp	Val	Val
			275			280						285			
Ala	Leu	Phe	Pro	Asn	Tyr	Asp	Thr	Arg	Thr	Tyr	Pro	Met	Glu	Thr	Lys
			290			295				300					
Ala	Gln	Leu	Thr	Arg	Glu	Val	Tyr	Thr	Asp	Pro	Leu	Gly	Ala	Val	Asn
305				310					315						320
Val	Ser	Ser	Ile	Gly	Ser	Trp	Tyr	Asp	Lys	Ala	Pro	Ser	Phe	Gly	Val
				325				330					335		
Ile	Glu	Ser	Ser	Val	Ile	Arg	Pro	Pro	His	Val	Phe	Asp	Tyr	Ile	Thr
			340					345					350		
Gly	Leu	Thr	Val	Tyr	Thr	Gln	Ser	Arg	Ser	Ile	Ser	Ser	Ala	Arg	Tyr
			355			360						365			
Ile	Arg	His	Trp	Ala	Gly	His	Gln	Ile	Ser	Tyr	His	Arg	Val	Ser	Arg
			370			375					380				
Gly	Ser	Asn	Leu	Gln	Gln	Met	Tyr	Gly	Thr	Asn	Gln	Asn	Leu	His	Ser
385				390						395				400	
Thr	Ser	Thr	Phe	Asp	Phe	Thr	Asn	Tyr	Asp	Ile	Tyr	Lys	Thr	Leu	Ser
				405					410				415		
Lys	Asp	Ala	Val	Leu	Leu	Asp	Ile	Val	Tyr	Pro	Gly	Tyr	Thr	Tyr	Ile
			420					425					430		
Phe	Phe	Gly	Met	Pro	Glu	Val	Glu	Phe	Phe	Met	Val	Asn	Gln	Leu	Asn
			435				440					445			
Asn	Thr	Arg	Lys	Thr	Leu	Lys	Tyr	Asn	Pro	Val	Ser	Lys	Asp	Ile	Ile
			450			455					460				
Ala	Ser	Thr	Arg	Asp	Ser	Glu	Leu	Glu	Leu	Pro	Pro	Glu	Thr	Ser	Asp
465				470						475				480	
Gln	Pro	Asn	Tyr	Glu	Ser	Tyr	Ser	His	Arg	Leu	Cys	His	Ile	Thr	Ser
				485					490				495		
Ile	Pro	Ala	Thr	Gly	Asn	Thr	Thr	Gly	Leu	Val	Pro	Val	Phe	Ser	Trp
			500					505					510		
Thr	His	Arg	Ser	Ala	Asp	Leu	Asn	Asn	Thr	Ile	Tyr	Ser	Asp	Lys	Ile
			515												

Ala Asp Ala Ile Thr Thr Val Asn Leu Ala Thr Asp Ser Ser Val Ala
625 630 635 640
Val Lys His Asn Val Gly Glu Asp Pro Asn Ser Thr Leu Ser Gly Ile
645 650 655
Val Tyr Val Asp Arg Ile Glu Phe Ile Pro Val Asp Glu Thr Tyr Glu
660 665 670
Ala Glu

<210> 45
<211> 2025
<212> DNA
<213> *Bacillus thuringiensis* (mutated)

<220>
<221> CDS
<222> (1)...(2025)

<400> 45
atg agt cca aat aat caa aat gaa tat gaa att ata gat gcg aca cct 48
Met Ser Pro Asn Asn Gln Asn Glu Tyr Glu Ile Ile Asp Ala Thr Pro
1 5 10 15
tct act tct gta tcc aat gat tct aac aga tac cct ttt gcg aat gag 96
Ser Thr Ser Val Ser Asn Asp Ser Asn Arg Tyr Pro Phe Ala Asn Glu
20 25 30
cca aca aat gcg cta caa aat atg gat tat aaa gat tat tta aaa atg 144
Pro Thr Asn Ala Leu Gln Asn Met Asp Tyr Lys Asp Tyr Leu Lys Met
35 40 45
tct gcg gga aat gct agt gaa tac cct ggt tca cct gaa gta ctt gtt 192
Ser Ala Gly Asn Ala Ser Glu Tyr Pro Gly Ser Pro Glu Val Leu Val
50 55 60
agc gga caa gat gca gct aag gcc gca att gat ata gta ggt aaa tta 240
Ser Gly Gln Asp Ala Ala Lys Ala Ala Ile Asp Ile Val Gly Lys Leu
65 70 75 80
cta tca ggt tta ggg gtc cca ttt gtt ggg ccg ata gtg agt ctt tat 288
Leu Ser Gly Leu Gly Val Pro Phe Val Gly Pro Ile Val Ser Leu Tyr
85 90 95
act caa ctt att gat att ctg tgg cct tca ggg gaa aag agt caa tgg 336
Thr Gln Leu Ile Asp Ile Leu Trp Pro Ser Gly Glu Lys Ser Gln Trp
100 105 110
gaa att ttt atg gaa caa gta gaa gaa ctc att aat caa aaa ata gca 384
Glu Ile Phe Met Glu Gln Val Glu Glu Leu Ile Asn Gln Lys Ile Ala
115 120 125
gaa tat gca agg aat aaa gcg ctt tcg gaa tta gaa gga tta ggt aat 432
Glu Tyr Ala Arg Asn Lys Ala Leu Ser Glu Leu Glu Gly Leu Gly Asn
130 135 140
aat tac caa tta tat cta act gcg ctt gaa gaa tgg gaa gaa aat cca 480

Asn Tyr Gln Leu Tyr Leu Thr Ala Leu Glu Glu Trp Glu Glu Asn Pro	
145 150 155 160	
aat ggt tcc cgg ttt cga agt cga ggt cca gcc tta cga gat gtg cga	528
Asn Gly Ser Arg Phe Arg Ser Arg Gly Pro Ala Leu Arg Asp Val Arg	
165 170 175	
aat cga ttt gaa atc ctg gat agt tta ttt acg caa tat atg cca tct	576
Asn Arg Phe Glu Ile Leu Asp Ser Leu Phe Thr Gln Tyr Met Pro Ser	
180 185 190	
ttt aga gtg aca aat ttt gaa gta cca ttc ctt act gta tat gca atg	624
Phe Arg Val Thr Asn Phe Glu Val Pro Phe Leu Thr Val Tyr Ala Met	
195 200 205	
gca gcc aac ctt cat tta ctg tta tta aag gac gcg tca att ttt gga	672
Ala Ala Asn Leu His Leu Leu Leu Leu Lys Asp Ala Ser Ile Phe Gly	
210 215 220	
gaa gaa tgg gga tgg tca aca act act att aat aac tat tat gat cgt	720
Glu Glu Trp Gly Trp Ser Thr Thr Thr Ile Asn Asn Tyr Tyr Asp Arg	
225 230 235 240	
caa atg aaa ctt act gca gaa tat tct gat cac tgt gta aag tgg tat	768
Gln Met Lys Leu Thr Ala Glu Tyr Ser Asp His Cys Val Lys Trp Tyr	
245 250 255	
gaa act ggt tta gca aaa tta aaa ggc acg agc gct aaa caa tgg gtt	816
Glu Thr Gly Leu Ala Lys Leu Lys Gly Thr Ser Ala Lys Gln Trp Val	
260 265 270	
gac tat aac caa ttc cgt aga gaa atg aca ctg gcg gtt tta gat gtt	864
Asp Tyr Asn Gln Phe Arg Arg Glu Met Thr Leu Ala Val Leu Asp Val	
275 280 285	
gtt gca tta ttc cca aat tat gac aca cgc acg tac cca atg gaa acg	912
Val Ala Leu Phe Pro Asn Tyr Asp Thr Arg Thr Tyr Pro Met Glu Thr	
290 295 300	
aaa gca caa cta aca agg gaa gta tat aca gat cca ctg ggc gcg gta	960
Lys Ala Gln Leu Thr Arg Glu Val Tyr Thr Asp Pro Leu Gly Ala Val	
305 310 315 320	
aac gtg tct tca att ggt tcc tgg tat gac aaa gca cct tct ttc gga	1008
Asn Val Ser Ser Ile Gly Ser Trp Tyr Asp Lys Ala Pro Ser Phe Gly	
325 330 335	
gtg ata gaa tca tcc gtt att cga cca ccc cat gta ttt gat tat ata	1056
Val Ile Glu Ser Ser Val Ile Arg Pro Pro His Val Phe Asp Tyr Ile	
340 345 350	
acg gga ctc aca gtg tat aca caa tca aga agc att tct tcc gct cgc	1104
Thr Gly Leu Thr Val Tyr Thr Gln Ser Arg Ser Ile Ser Ser Ala Arg	
355 360 365	
tat ata aga cat tgg gct ggt cat caa ata agc tac cat cgt gtc agt	1152
Tyr Ile Arg His Trp Ala Gly His Gln Ile Ser Tyr His Arg Val Ser	

370	375	380	
agg ggt agt aat ctt caa caa atg tat gga act aat caa aat cta cac			1200
Arg Gly Ser Asn Leu Gln Gln Met Tyr Gly Thr Asn Gln Asn Leu His			
385	390	395	400
agc act agt acc ttt gat ttt acg aat tat gat att tac aag act cta			1248
Ser Thr Ser Thr Phe Asp Phe Thr Asn Tyr Asp Ile Tyr Lys Thr Leu			
	405	410	415
tca aag gat gca gta ctc ctt gat att gtt tac cct ggt tat acg tat			1296
Ser Lys Asp Ala Val Leu Leu Asp Ile Val Tyr Pro Gly Tyr Thr Tyr			
	420	425	430
ata ttt ttt gga atg cca gaa gtc gag ttt ttc atg gta aac caa ttg			1344
Ile Phe Phe Gly Met Pro Glu Val Glu Phe Phe Met Val Asn Gln Leu			
	435	440	445
aat aat acc aga aag acg tta aag tat aat cca gtt tcc aaa gat att			1392
Asn Asn Thr Arg Lys Thr Leu Lys Tyr Asn Pro Val Ser Lys Asp Ile			
	450	455	460
ata gcg agt aca aga gat tcg gaa tta gaa tta cct cca gaa act tca			1440
Ile Ala Ser Thr Arg Asp Ser Glu Leu Glu Leu Pro Pro Glu Thr Ser			
	465	470	475
gat caa cca aat tat gag tca tat agc cat aga tta tgt cat atc aca			1488
Asp Gln Pro Asn Tyr Glu Ser Tyr Ser His Arg Leu Cys His Ile Thr			
	485	490	495
agt att ccc gcg acg ggt aac act acc gga tta gta cct gta ttt tct			1536
Ser Ile Pro Ala Thr Gly Asn Thr Thr Gly Leu Val Pro Val Phe Ser			
	500	505	510
tgg aca cat cga agt gca gat tta aac aat aca ata tat tca gat aaa			1584
Trp Thr His Arg Ser Ala Asp Leu Asn Asn Thr Ile Tyr Ser Asp Lys			
	515	520	525
atc act caa att ccg gcc gtt aaa tgt tgg gat aat tta ccg ttt gtt			1632
Ile Thr Gln Ile Pro Ala Val Lys Cys Trp Asp Asn Leu Pro Phe Val			
	530	535	540
cca gtg gta aaa gga cca gga cat aca gga ggg gat tta tta cag tat			1680
Pro Val Val Lys Gly Pro Gly His Thr Gly Gly Asp Leu Leu Gln Tyr			
	545	550	555
aat aga agt act ggt tct gta gga acc tta ttt cta gct cga tat ggc			1728
Asn Arg Ser Thr Gly Ser Val Gly Thr Leu Phe Leu Ala Arg Tyr Gly			
	565	570	575
cta gca tta gaa aaa gca ggg aaa tat cgt gta aga ctg aga tat gct			1776
Leu Ala Leu Glu Lys Ala Gly Lys Tyr Arg Val Arg Leu Arg Tyr Ala			
	580	585	590
act gat gca gat att gta ttg cat gta aac gat gct cag att cag atg			1824
Thr Asp Ala Asp Ile Val Leu His Val Asn Asp Ala Gln Ile Gln Met			
	595	600	605

cca aaa aca atg aac cca ggt gag gat ctg aca tct aaa act ttt aaa	1872
Pro Lys Thr Met Asn Pro Gly Glu Asp Leu Thr Ser Lys Thr Phe Lys	
610 615 620	
gtt gca gat gct atc aca aca gtt aat tta gca aca gat agt tcg gtt	1920
Val Ala Asp Ala Ile Thr Thr Val Asn Leu Ala Thr Asp Ser Ser Val	
625 630 635 640	
gca gtt aaa cat aat gta ggt gaa gac cct aat tca aca tta tct ggt	1968
Ala Val Lys His Asn Val Gly Glu Asp Pro Asn Ser Thr Leu Ser Gly	
645 650 655	
ata gtt tac gtt gac cga atc gaa ttc atc cca gta gat gag aca tat	2016
Ile Val Tyr Val Asp Arg Ile Glu Phe Ile Pro Val Asp Glu Thr Tyr	
660 665 670	
gaa gcg gaa	2025
Glu Ala Glu	
675	

<210> 46
 <211> 675
 <212> PRT
 <213> *Bacillus thuringiensis* (mutated)

<400> 46

Met Ser Pro Asn Asn Gln Asn Glu Tyr Glu Ile Ile Asp Ala Thr Pro	
1 5 10 15	
Ser Thr Ser Val Ser Asn Asp Ser Asn Arg Tyr Pro Phe Ala Asn Glu	
20 25 30	
Pro Thr Asn Ala Leu Gln Asn Met Asp Tyr Lys Asp Tyr Leu Lys Met	
35 40 45	
Ser Ala Gly Asn Ala Ser Glu Tyr Pro Gly Ser Pro Glu Val Leu Val	
50 55 60	
Ser Gly Gln Asp Ala Ala Lys Ala Ala Ile Asp Ile Val Gly Lys Leu	
65 70 75 80	
Leu Ser Gly Leu Gly Val Pro Phe Val Gly Pro Ile Val Ser Leu Tyr	
85 90 95	
Thr Gln Leu Ile Asp Ile Leu Trp Pro Ser Gly Glu Lys Ser Gln Trp	
100 105 110	
Glu Ile Phe Met Glu Gln Val Glu Glu Leu Ile Asn Gln Lys Ile Ala	
115 120 125	
Glu Tyr Ala Arg Asn Lys Ala Leu Ser Glu Leu Glu Gly Leu Gly Asn	
130 135 140	
Asn Tyr Gln Leu Tyr Leu Thr Ala Leu Glu Glu Trp Glu Glu Asn Pro	
145 150 155 160	
Asn Gly Ser Arg Phe Arg Ser Arg Gly Pro Ala Leu Arg Asp Val Arg	
165 170 175	
Asn Arg Phe Glu Ile Leu Asp Ser Leu Phe Thr Gln Tyr Met Pro Ser	
180 185 190	
Phe Arg Val Thr Asn Phe Glu Val Pro Phe Leu Thr Val Tyr Ala Met	
195 200 205	
Ala Ala Asn Leu His Leu Leu Leu Leu Lys Asp Ala Ser Ile Phe Gly	
210 215 220	
Glu Glu Trp Gly Trp Ser Thr Thr Thr Ile Asn Asn Tyr Tyr Asp Arg	

225					230					235				240	
Gln	Met	Lys	Leu	Thr	Ala	Glu	Tyr	Ser	Asp	His	Cys	Val	Lys	Trp	Tyr
				245					250					255	
Glu	Thr	Gly	Leu	Ala	Lys	Leu	Lys	Gly	Thr	Ser	Ala	Lys	Gln	Trp	Val
			260					265					270		
Asp	Tyr	Asn	Gln	Phe	Arg	Arg	Glu	Met	Thr	Leu	Ala	Val	Leu	Asp	Val
		275					280					285			
Val	Ala	Leu	Phe	Pro	Asn	Tyr	Asp	Thr	Arg	Thr	Tyr	Pro	Met	Glu	Thr
		290				295					300				
Lys	Ala	Gln	Leu	Thr	Arg	Glu	Val	Tyr	Thr	Asp	Pro	Leu	Gly	Ala	Val
305					310					315				320	
Asn	Val	Ser	Ser	Ile	Gly	Ser	Trp	Tyr	Asp	Lys	Ala	Pro	Ser	Phe	Gly
			325						330					335	
Val	Ile	Glu	Ser	Ser	Val	Ile	Arg	Pro	Pro	His	Val	Phe	Asp	Tyr	Ile
		340						345					350		
Thr	Gly	Leu	Thr	Val	Tyr	Thr	Gln	Ser	Arg	Ser	Ile	Ser	Ser	Ala	Arg
		355					360						365		
Tyr	Ile	Arg	His	Trp	Ala	Gly	His	Gln	Ile	Ser	Tyr	His	Arg	Val	Ser
		370				375					380				
Arg	Gly	Ser	Asn	Leu	Gln	Gln	Met	Tyr	Gly	Thr	Asn	Gln	Asn	Leu	His
385					390					395				400	
Ser	Thr	Ser	Thr	Phe	Asp	Phe	Thr	Asn	Tyr	Asp	Ile	Tyr	Lys	Thr	Leu
			405						410					415	
Ser	Lys	Asp	Ala	Val	Leu	Leu	Asp	Ile	Val	Tyr	Pro	Gly	Tyr	Thr	Tyr
			420					425					430		
Ile	Phe	Phe	Gly	Met	Pro	Glu	Val	Glu	Phe	Phe	Met	Val	Asn	Gln	Leu
		435					440					445			
Asn	Asn	Thr	Arg	Lys	Thr	Leu	Lys	Tyr	Asn	Pro	Val	Ser	Lys	Asp	Ile
		450				455					460				
Ile	Ala	Ser	Thr	Arg	Asp	Ser	Glu	Leu	Glu	Leu	Pro	Pro	Glu	Thr	Ser
465					470					475				480	
Asp	Gln	Pro	Asn	Tyr	Glu	Ser	Tyr	Ser	His	Arg	Leu	Cys	His	Ile	Thr
			485						490					495	
Ser	Ile	Pro	Ala	Thr	Gly	Asn	Thr	Thr	Gly	Leu	Val	Pro	Val	Phe	Ser
			500					505					510		
Trp	Thr	His	Arg	Ser	Ala	Asp	Leu	Asn	Asn	Thr	Ile	Tyr	Ser	Asp	Lys
		515					520					525			
Ile	Thr	Gln	Ile	Pro	Ala	Val	Lys	Cys	Trp	Asp	Asn	Leu	Pro	Phe	Val
		530				535					540				
Pro	Val	Val	Lys	Gly	Pro	Gly	His	Thr	Gly	Gly	Asp	Leu	Leu	Gln	Tyr
545					550					555				560	
Asn	Arg	Ser	Thr	Gly	Ser	Val	Gly	Thr	Leu	Phe	Leu	Ala	Arg	Tyr	Gly
			565					570					575		
Leu	Ala	Leu	Glu	Lys	Ala	Gly	Lys	Tyr	Arg	Val	Arg	Leu	Arg	Tyr	Ala
		580						585					590		
Thr	Asp	Ala	Asp	Ile	Val	Leu	His	Val	Asn	Asp	Ala	Gln	Ile	Gln	Met
		595					600					605			
Pro	Lys	Thr	Met	Asn	Pro	Gly	Glu	Asp	Leu	Thr	Ser	Lys	Thr	Phe	Lys
		610				615					620				
Val	Ala	Asp	Ala	Ile	Thr	Thr	Val	Asn	Leu	Ala	Thr	Asp	Ser	Ser	Val
625					630					635				640	
Ala	Val	Lys	His	Asn	Val	Gly	Glu	Asp	Pro	Asn	Ser	Thr	Leu	Ser	Gly
			645					650					655		
Ile	Val	Tyr	Val	Asp	Arg	Ile	Glu	Phe	Ile	Pro	Val	Asp	Glu	Thr	Tyr
			660					665					670		
Glu	Ala	Glu													
		675													

<210> 47
 <211> 2025
 <212> DNA
 <213> Bacillus thuringiensis (mutated)

<220>
 <221> CDS
 <222> (1)...(2025)

<400> 47
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 1 5 10 15
 tct act tct gta tcc aat gat tct aac aga tac cct ttt gcg aat gag 96
 Ser Thr Ser Val Ser Asn Asp Ser Asn Arg Tyr Pro Phe Ala Asn Glu
 20 25 30
 cca aca aat gcg cta caa aat atg gat tat aaa gat tat tta aaa atg 144
 Pro Thr Asn Ala Leu Gln Asn Met Asp Tyr Lys Asp Tyr Leu Lys Met
 35 40 45
 tct gcg gga aat gct agt gaa tac cct ggt tca cct gaa gta ctt gtt 192
 Ser Ala Gly Asn Ala Ser Glu Tyr Pro Gly Ser Pro Glu Val Leu Val
 50 55 60
 agc gga caa gat gca gct aag gcc gca att gat ata gta ggt aaa tta 240
 Ser Gly Gln Asp Ala Ala Lys Ala Ala Ile Asp Ile Val Gly Lys Leu
 65 70 75 80
 cta tca ggt tta ggg gtc cca ttt gtt ggg ccg ata gtg agt ctt tat 288
 Leu Ser Gly Leu Gly Val Pro Phe Val Gly Pro Ile Val Ser Leu Tyr
 85 90 95
 act caa ctt att gat att ctg tgg cct tca ggg gaa aag agt caa tgg 336
 Thr Gln Leu Ile Asp Ile Leu Trp Pro Ser Gly Glu Lys Ser Gln Trp
 100 105 110
 gaa att ttt atg gaa caa gta gaa gaa ctc att aat caa aaa ata gca 384
 Glu Ile Phe Met Glu Gln Val Glu Glu Leu Ile Asn Gln Lys Ile Ala
 115 120 125
 gaa tat gca agg aat aaa gcg ctt tcg gaa tta gaa gga tta ggt aat 432
 Glu Tyr Ala Arg Asn Lys Ala Leu Ser Glu Leu Glu Gly Leu Gly Asn
 130 135 140
 aat tac caa tta tat cta act gcg ctt gaa gaa tgg gaa gaa aat cca 480
 Asn Tyr Gln Leu Tyr Leu Thr Ala Leu Glu Glu Trp Glu Glu Asn Pro
 145 150 155 160
 ttt cga agt cga ggt cca aat ggt tcc cgg gcc tta cga gat gtg cga 528
 Phe Arg Ser Arg Gly Pro Asn Gly Ser Arg Ala Leu Arg Asp Val Arg
 165 170 175
 aat cga ttt gaa atc ctg gat agt tta ttt acg caa tat atg cca tct 576

Asn	Arg	Phe	Glu	Ile	Leu	Asp	Ser	Leu	Phe	Thr	Gln	Tyr	Met	Pro	Ser		
			180					185					190				
ttt	aga	gtg	aca	aat	ttt	gaa	gta	cca	ttc	ctt	act	gta	tat	gca	atg	624	
Phe	Arg	Val	Thr	Asn	Phe	Glu	Val	Pro	Phe	Leu	Thr	Val	Tyr	Ala	Met		
		195				200					205						
gca	gcc	aac	ctt	cat	tta	ctg	tta	tta	aag	gac	gcg	tca	att	ttt	gga	672	
Ala	Ala	Asn	Leu	His	Leu	Leu	Leu	Leu	Lys	Asp	Ala	Ser	Ile	Phe	Gly		
	210				215					220							
gaa	gaa	tgg	gga	tgg	tca	aca	act	act	att	aat	aac	tat	tat	gat	cgt	720	
Glu	Glu	Trp	Gly	Trp	Ser	Thr	Thr	Thr	Ile	Asn	Asn	Tyr	Tyr	Asp	Arg		
225					230					235					240		
caa	atg	aaa	ctt	act	gca	gaa	tat	tct	gat	cac	tgt	gta	aag	tgg	tat	768	
Gln	Met	Lys	Leu	Thr	Ala	Glu	Tyr	Ser	Asp	His	Cys	Val	Lys	Trp	Tyr		
			245					250						255			
gaa	act	ggt	tta	gca	aaa	tta	aaa	ggc	acg	agc	gct	aaa	caa	tgg	gtt	816	
Glu	Thr	Gly	Leu	Ala	Lys	Leu	Lys	Gly	Thr	Ser	Ala	Lys	Gln	Trp	Val		
			260					265					270				
gac	tat	aac	caa	ttc	cgt	aga	gaa	atg	aca	ctg	gcg	ggt	tta	gat	gtt	864	
Asp	Tyr	Asn	Gln	Phe	Arg	Arg	Glu	Met	Thr	Leu	Ala	Val	Leu	Asp	Val		
		275				280						285					
gtt	gca	tta	ttc	cca	aat	tat	gac	aca	cgc	acg	tac	cca	atg	gaa	acg	912	
Val	Ala	Leu	Phe	Pro	Asn	Tyr	Asp	Thr	Arg	Thr	Tyr	Pro	Met	Glu	Thr		
	290				295						300						
aaa	gca	caa	cta	aca	agg	gaa	gta	tat	aca	gat	cca	ctg	ggc	gcg	gta	960	
Lys	Ala	Gln	Leu	Thr	Arg	Glu	Val	Tyr	Thr	Asp	Pro	Leu	Gly	Ala	Val		
305				310						315					320		
aac	gtg	tct	tca	att	ggt	tcc	tgg	tat	gac	aaa	gca	cct	tct	ttc	gga	1008	
Asn	Val	Ser	Ser	Ile	Gly	Ser	Trp	Tyr	Asp	Lys	Ala	Pro	Ser	Phe	Gly		
			325					330						335			
gtg	ata	gaa	tca	tcc	gtt	att	cga	cca	ccc	cat	gta	ttt	gat	tat	ata	1056	
Val	Ile	Glu	Ser	Ser	Val	Ile	Arg	Pro	Pro	His	Val	Phe	Asp	Tyr	Ile		
			340					345					350				
acg	gga	ctc	aca	gtg	tat	aca	caa	tca	aga	agc	att	tct	tcc	gct	cgc	1104	
Thr	Gly	Leu	Thr	Val	Tyr	Thr	Gln	Ser	Arg	Ser	Ile	Ser	Ser	Ala	Arg		
		355				360						365					
tat	ata	aga	cat	tgg	gct	ggt	cat	caa	ata	agc	tac	cat	cgt	gtc	agt	1152	
Tyr	Ile	Arg	His	Trp	Ala	Gly	His	Gln	Ile	Ser	Tyr	His	Arg	Val	Ser		
	370				375						380						
agg	ggt	agt	aat	ctt	caa	caa	atg	tat	gga	act	aat	caa	aat	cta	cac	1200	
Arg	Gly	Ser	Asn	Leu	Gln	Gln	Met	Tyr	Gly	Thr	Asn	Gln	Asn	Leu	His		
385				390					395					400			
agc	act	agt	acc	ttt	gat	ttt	acg	aat	tat	gat	att	tac	aag	act	cta	1248	
Ser	Thr	Ser	Thr	Phe	Asp	Phe	Thr	Asn	Tyr	Asp	Ile	Tyr	Lys	Thr	Leu		

405										410					415					
tca	aag	gat	gca	gta	ctc	ctt	gat	att	gtt	tac	cct	ggg	tat	acg	tat	1296				
Ser	Lys	Asp	Ala	Val	Leu	Leu	Asp	Ile	Val	Tyr	Pro	Gly	Tyr	Thr	Tyr					
			420				425				430									
ata	ttt	ttt	gga	atg	cca	gaa	gtc	gag	ttt	ttc	atg	gta	aac	caa	ttg	1344				
Ile	Phe	Phe	Gly	Met	Pro	Glu	Val	Glu	Phe	Phe	Met	Val	Asn	Gln	Leu					
			435				440				445									
aat	aat	acc	aga	aag	acg	tta	aag	tat	aat	cca	gtt	tcc	aaa	gat	att	1392				
Asn	Asn	Thr	Arg	Lys	Thr	Leu	Lys	Tyr	Asn	Pro	Val	Ser	Lys	Asp	Ile					
			450				455				460									
ata	gcg	agt	aca	aga	gat	tcg	gaa	tta	gaa	tta	cct	cca	gaa	act	tca	1440				
Ile	Ala	Ser	Thr	Arg	Asp	Ser	Glu	Leu	Glu	Leu	Pro	Pro	Glu	Thr	Ser					
465				470				475				480								
gat	caa	cca	aat	tat	gag	tca	tat	agc	cat	aga	tta	tgt	cat	atc	aca	1488				
Asp	Gln	Pro	Asn	Tyr	Glu	Ser	Tyr	Ser	His	Arg	Leu	Cys	His	Ile	Thr					
			485				490				495									
agt	att	ccc	gcg	acg	ggg	aac	act	acc	gga	tta	gta	cct	gta	ttt	tct	1536				
Ser	Ile	Pro	Ala	Thr	Gly	Asn	Thr	Thr	Gly	Leu	Val	Pro	Val	Phe	Ser					
			500				505				510									
tgg	aca	cat	cga	agt	gca	gat	tta	aac	aat	aca	ata	tat	tca	gat	aaa	1584				
Trp	Thr	His	Arg	Ser	Ala	Asp	Leu	Asn	Asn	Thr	Ile	Tyr	Ser	Asp	Lys					
			515				520				525									
atc	act	caa	att	ccg	gcc	gtt	aaa	tgt	tgg	gat	aat	tta	ccg	ttt	gtt	1632				
Ile	Thr	Gln	Ile	Pro	Ala	Val	Lys	Cys	Trp	Asp	Asn	Leu	Pro	Phe	Val					
			530				535				540									
cca	gtg	gta	aaa	gga	cca	gga	cat	aca	gga	ggg	gat	tta	tta	cag	tat	1680				
Pro	Val	Val	Lys	Gly	Pro	Gly	His	Thr	Gly	Gly	Asp	Leu	Leu	Gln	Tyr					
545				550				555				560								
aat	aga	agt	act	ggg	tct	gta	gga	acc	tta	ttt	cta	gct	cga	tat	ggc	1728				
Asn	Arg	Ser	Thr	Gly	Ser	Val	Gly	Thr	Leu	Phe	Leu	Ala	Arg	Tyr	Gly					
			565				570				575									
cta	gca	tta	gaa	aaa	gca	ggg	aaa	tat	cgt	gta	aga	ctg	aga	tat	gct	1776				
Leu	Ala	Leu	Glu	Lys	Ala	Gly	Lys	Tyr	Arg	Val	Arg	Leu	Arg	Tyr	Ala					
			580				585				590									
act	gat	gca	gat	att	gta	ttg	cat	gta	aac	gat	gct	cag	att	cag	atg	1824				
Thr	Asp	Ala	Asp	Ile	Val	Leu	His	Val	Asn	Asp	Ala	Gln	Ile	Gln	Met					
			595				600				605									
cca	aaa	aca	atg	aac	cca	ggg	gag	gat	ctg	aca	tct	aaa	act	ttt	aaa	1872				
Pro	Lys	Thr	Met	Asn	Pro	Gly	Glu	Asp	Leu	Thr	Ser	Lys	Thr	Phe	Lys					
			610				615				620									
gtt	gca	gat	gct	atc	aca	aca	gtt	aat	tta	gca	aca	gat	agt	tcg	gtt	1920				
Val	Ala	Asp	Ala	Ile	Thr	Thr	Val	Asn	Leu	Ala	Thr	Asp	Ser	Ser	Val					
625				630				635				640								

gca gtt aaa cat aat gta ggt gaa gac cct aat tca aca tta tct ggt 1968
Ala Val Lys His Asn Val Gly Glu Asp Pro Asn Ser Thr Leu Ser Gly
645 650 655

ata gtt tac gtt gac cga atc gaa ttc atc cca gta gat gag aca tat 2016
Ile Val Tyr Val Asp Arg Ile Glu Phe Ile Pro Val Asp Glu Thr Tyr
660 665 670

gaa gcg gaa 2025
Glu Ala Glu
675

<210> 48
<211> 675
<212> PRT
<213> Bacillus thuringiensis (mutated)

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20 25 30
Pro Thr Asn Ala Leu Gln Asn Met Asp Tyr Lys Asp Tyr Leu Lys Met
35 40 45
Ser Ala Gly Asn Ala Ser Glu Tyr Pro Gly Ser Pro Glu Val Leu Val
50 55 60
Ser Gly Gln Asp Ala Ala Lys Ala Ala Ile Asp Ile Val Gly Lys Leu
65 70 75 80
Leu Ser Gly Leu Gly Val Pro Phe Val Gly Pro Ile Val Ser Leu Tyr
85 90 95
Thr Gln Leu Ile Asp Ile Leu Trp Pro Ser Gly Glu Lys Ser Gln Trp
100 105 110
Glu Ile Phe Met Glu Gln Val Glu Glu Leu Ile Asn Gln Lys Ile Ala
115 120 125
Glu Tyr Ala Arg Asn Lys Ala Leu Ser Glu Leu Glu Gly Leu Gly Asn
130 135 140
Asn Tyr Gln Leu Tyr Leu Thr Ala Leu Glu Glu Trp Glu Glu Asn Pro
145 150 155 160
Phe Arg Ser Arg Gly Pro Asn Gly Ser Arg Ala Leu Arg Asp Val Arg
165 170 175
Asn Arg Phe Glu Ile Leu Asp Ser Leu Phe Thr Gln Tyr Met Pro Ser
180 185 190
Phe Arg Val Thr Asn Phe Glu Val Pro Phe Leu Thr Val Tyr Ala Met
195 200 205
Ala Ala Asn Leu His Leu Leu Leu Leu Lys Asp Ala Ser Ile Phe Gly
210 215 220
Glu Glu Trp Gly Trp Ser Thr Thr Thr Ile Asn Asn Tyr Tyr Asp Arg
225 230 235 240
Gln Met Lys Leu Thr Ala Glu Tyr Ser Asp His Cys Val Lys Trp Tyr
245 250 255
Glu Thr Gly Leu Ala Lys Leu Lys Gly Thr Ser Ala Lys Gln Trp Val
260 265 270
Asp Tyr Asn Gln Phe Arg Arg Glu Met Thr Leu Ala Val Leu Asp Val
275 280 285
Val Ala Leu Phe Pro Asn Tyr Asp Thr Arg Thr Tyr Pro Met Glu Thr

290		295		300											
Lys	Ala	Gln	Leu	Thr	Arg	Glu	Val	Tyr	Thr	Asp	Pro	Leu	Gly	Ala	Val
305					310					315					320
Asn	Val	Ser	Ser	Ile	Gly	Ser	Trp	Tyr	Asp	Lys	Ala	Pro	Ser	Phe	Gly
				325					330					335	
Val	Ile	Glu	Ser	Ser	Val	Ile	Arg	Pro	Pro	His	Val	Phe	Asp	Tyr	Ile
				340					345					350	
Thr	Gly	Leu	Thr	Val	Tyr	Thr	Gln	Ser	Arg	Ser	Ile	Ser	Ser	Ala	Arg
				355					360					365	
Tyr	Ile	Arg	His	Trp	Ala	Gly	His	Gln	Ile	Ser	Tyr	His	Arg	Val	Ser
				370					375					380	
Arg	Gly	Ser	Asn	Leu	Gln	Gln	Met	Tyr	Gly	Thr	Asn	Gln	Asn	Leu	His
385					390					395					400
Ser	Thr	Ser	Thr	Phe	Asp	Phe	Thr	Asn	Tyr	Asp	Ile	Tyr	Lys	Thr	Leu
				405					410					415	
Ser	Lys	Asp	Ala	Val	Leu	Leu	Asp	Ile	Val	Tyr	Pro	Gly	Tyr	Thr	Tyr
				420					425					430	
Ile	Phe	Phe	Gly	Met	Pro	Glu	Val	Glu	Phe	Phe	Met	Val	Asn	Gln	Leu
				435					440					445	
Asn	Asn	Thr	Arg	Lys	Thr	Leu	Lys	Tyr	Asn	Pro	Val	Ser	Lys	Asp	Ile
				450					455					460	
Ile	Ala	Ser	Thr	Arg	Asp	Ser	Glu	Leu	Glu	Leu	Pro	Pro	Glu	Thr	Ser
465					470					475					480
Asp	Gln	Pro	Asn	Tyr	Glu	Ser	Tyr	Ser	His	Arg	Leu	Cys	His	Ile	Thr
				485					490					495	
Ser	Ile	Pro	Ala	Thr	Gly	Asn	Thr	Thr	Gly	Leu	Val	Pro	Val	Phe	Ser
				500					505					510	
Trp	Thr	His	Arg	Ser	Ala	Asp	Leu	Asn	Asn	Thr	Ile	Tyr	Ser	Asp	Lys
				515					520					525	
Ile	Thr	Gln	Ile	Pro	Ala	Val	Lys	Cys	Trp	Asp	Asn	Leu	Pro	Phe	Val
				530					535					540	
Pro	Val	Val	Lys	Gly	Pro	Gly	His	Thr	Gly	Gly	Asp	Leu	Leu	Gln	Tyr
545					550					555					560
Asn	Arg	Ser	Thr	Gly	Ser	Val	Gly	Thr	Leu	Phe	Leu	Ala	Arg	Tyr	Gly
				565					570					575	
Leu	Ala	Leu	Glu	Lys	Ala	Gly	Lys	Tyr	Arg	Val	Arg	Leu	Arg	Tyr	Ala
				580					585					590	
Thr	Asp	Ala	Asp	Ile	Val	Leu	His	Val	Asn	Asp	Ala	Gln	Ile	Gln	Met
				595					600					605	
Pro	Lys	Thr	Met	Asn	Pro	Gly	Glu	Asp	Leu	Thr	Ser	Lys	Thr	Phe	Lys
				610					615					620	
Val	Ala	Asp	Ala	Ile	Thr	Thr	Val	Asn	Leu	Ala	Thr	Asp	Ser	Ser	Val
625					630					635					640
Ala	Val	Lys	His	Asn	Val	Gly	Glu	Asp	Pro	Asn	Ser	Thr	Leu	Ser	Gly
				645					650					655	
Ile	Val	Tyr	Val	Asp	Arg	Ile	Glu	Phe	Ile	Pro	Val	Asp	Glu	Thr	Tyr
				660					665					670	
Glu	Ala	Glu													
				675											

<210> 49
 <211> 2022
 <212> DNA
 <213> Bacillus thuringiensis (mutated)

 <220>

<221> CDS

<222> (1)...(2022)

<400> 49

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tct act tct gta tcc aat gat tct aac aga tac cct ttt gcg aat gag	96
Ser Thr Ser Val Ser Asn Asp Ser Asn Arg Tyr Pro Phe Ala Asn Glu	
20 25 30	
cca aca aat gcg cta caa aat atg gat tat aaa gat tat tta aaa atg	144
Pro Thr Asn Ala Leu Gln Asn Met Asp Tyr Lys Asp Tyr Leu Lys Met	
35 40 45	
tct gcg gga aat gct agt gaa tac cct ggt tca cct gaa gta ctt gtt	192
Ser Ala Gly Asn Ala Ser Glu Tyr Pro Gly Ser Pro Glu Val Leu Val	
50 55 60	
agc gga caa gat gca gct aag gcc gca att gat ata gta ggt aaa tta	240
Ser Gly Gln Asp Ala Ala Lys Ala Ala Ile Asp Ile Val Gly Lys Leu	
65 70 75 80	
cta tca ggt tta ggg gtc cca ttt gtt ggg ccg ata gtg agt ctt tat	288
Leu Ser Gly Leu Gly Val Pro Phe Val Gly Pro Ile Val Ser Leu Tyr	
85 90 95	
act caa ctt att gat att ctg tgg cct tca ggg gaa aag agt caa tgg	336
Thr Gln Leu Ile Asp Ile Leu Trp Pro Ser Gly Glu Lys Ser Gln Trp	
100 105 110	
gaa att ttt atg gaa caa gta gaa gaa ctc att aat caa aaa ata gca	384
Glu Ile Phe Met Glu Gln Val Glu Glu Leu Ile Asn Gln Lys Ile Ala	
115 120 125	
gaa tat gca agg aat aaa gcg ctt tcg gaa tta gaa gga tta ggt aat	432
Glu Tyr Ala Arg Asn Lys Ala Leu Ser Glu Leu Glu Gly Leu Gly Asn	
130 135 140	
aat tac caa tta tat cta act gcg ctt gaa gaa tgg gaa gaa aat cca	480
Asn Tyr Gln Leu Tyr Leu Thr Ala Leu Glu Glu Trp Glu Glu Asn Pro	
145 150 155 160	
aat ggt tcc cgg ttt cga agt cga caa gcc tta cga gat gtg cga aat	528
Asn Gly Ser Arg Phe Arg Ser Arg Gln Ala Leu Arg Asp Val Arg Asn	
165 170 175	
cga ttt gaa atc ctg gat agt tta ttt acg caa tat atg cca tct ttt	576
Arg Phe Glu Ile Leu Asp Ser Leu Phe Thr Gln Tyr Met Pro Ser Phe	
180 185 190	
aga gtg aca aat ttt gaa gta cca ttc ctt act gta tat gca atg gca	624
Arg Val Thr Asn Phe Glu Val Pro Phe Leu Thr Val Tyr Ala Met Ala	
195 200 205	
gcc aac ctt cat tta ctg tta tta aag gac gcg tca att ttt gga gaa	672

Ala Asn Leu His Leu Leu Leu Leu Lys Asp Ala Ser Ile Phe Gly Glu	
210 215 220	
gaa tgg gga tgg tca aca act act att aat aac tat tat gat cgt caa	720
Glu Trp Gly Trp Ser Thr Thr Thr Ile Asn Asn Tyr Tyr Asp Arg Gln	
225 230 235 240	
atg aaa ctt act gca gaa tat tct gat cac tgt gta aag tgg tat gaa	768
Met Lys Leu Thr Ala Glu Tyr Ser Asp His Cys Val Lys Trp Tyr Glu	
245 250 255	
act ggt tta gca aaa tta aaa ggc acg agc gct aaa caa tgg gtt gac	816
Thr Gly Leu Ala Lys Leu Lys Gly Thr Ser Ala Lys Gln Trp Val Asp	
260 265 270	
tat aac caa ttc cgt aga gaa atg aca ctg gcg gtt tta gat gtt gtt	864
Tyr Asn Gln Phe Arg Arg Glu Met Thr Leu Ala Val Leu Asp Val Val	
275 280 285	
gca tta ttc cca aat tat gac aca cgc acg tac cca atg gaa acg aaa	912
Ala Leu Phe Pro Asn Tyr Asp Thr Arg Thr Tyr Pro Met Glu Thr Lys	
290 295 300	
gca caa cta aca agg gaa gta tat aca gat cca ctg ggc gcg gta aac	960
Ala Gln Leu Thr Arg Glu Val Tyr Thr Asp Pro Leu Gly Ala Val Asn	
305 310 315 320	
gtg tct tca att ggt tcc tgg tat gac aaa gca cct tct ttc gga gtg	1008
Val Ser Ser Ile Gly Ser Trp Tyr Asp Lys Ala Pro Ser Phe Gly Val	
325 330 335	
ata gaa tca tcc gtt att cga cca ccc cat gta ttt gat tat ata acg	1056
Ile Glu Ser Ser Val Ile Arg Pro Pro His Val Phe Asp Tyr Ile Thr	
340 345 350	
gga ctc aca gtg tat aca caa tca aga agc att tct tcc gct cgc tat	1104
Gly Leu Thr Val Tyr Thr Gln Ser Arg Ser Ile Ser Ser Ala Arg Tyr	
355 360 365	
ata aga cat tgg gct ggt cat caa ata agc tac cat cgt gtc agt agg	1152
Ile Arg His Trp Ala Gly His Gln Ile Ser Tyr His Arg Val Ser Arg	
370 375 380	
ggt agt aat ctt caa caa atg tat gga act aat caa aat cta cac agc	1200
Gly Ser Asn Leu Gln Gln Met Tyr Gly Thr Asn Gln Asn Leu His Ser	
385 390 395 400	
act agt acc ttt gat ttt acg aat tat gat att tac aag act cta tca	1248
Thr Ser Thr Phe Asp Phe Thr Asn Tyr Asp Ile Tyr Lys Thr Leu Ser	
405 410 415	
aag gat gca gta ctc ctt gat att gtt tac cct ggt tat acg tat ata	1296
Lys Asp Ala Val Leu Leu Asp Ile Val Tyr Pro Gly Tyr Thr Tyr Ile	
420 425 430	
ttt ttt gga atg cca gaa gtc gag ttt ttc atg gta aac caa ttg aat	1344
Phe Phe Gly Met Pro Glu Val Glu Phe Phe Met Val Asn Gln Leu Asn	

435	440	445	
aat acc aga aag acg tta aag tat aat cca gtt tcc aaa gat att ata			1392
Asn Thr Arg Lys Thr Leu Lys Tyr Asn Pro Val Ser Lys Asp Ile Ile			
450	455	460	
gcg agt aca aga gat tcg gaa tta gaa tta cct cca gaa act tca gat			1440
Ala Ser Thr Arg Asp Ser Glu Leu Glu Leu Pro Pro Glu Thr Ser Asp			
465	470	475	480
caa cca aat tat gag tca tat agc cat aga tta tgt cat atc aca agt			1488
Gln Pro Asn Tyr Glu Ser Tyr Ser His Arg Leu Cys His Ile Thr Ser			
	485	490	495
att ccc gcg acg ggt aac act acc gga tta gta cct gta ttt tct tgg			1536
Ile Pro Ala Thr Gly Asn Thr Thr Gly Leu Val Pro Val Phe Ser Trp			
	500	505	510
aca cat cga agt gca gat tta aac aat aca ata tat tca gat aaa atc			1584
Thr His Arg Ser Ala Asp Leu Asn Asn Thr Ile Tyr Ser Asp Lys Ile			
	515	520	525
act caa att ccg gcc gtt aaa tgt tgg gat aat tta ccg ttt gtt cca			1632
Thr Gln Ile Pro Ala Val Lys Cys Trp Asp Asn Leu Pro Phe Val Pro			
	530	535	540
gtg gta aaa gga cca gga cat aca gga ggg gat tta tta cag tat aat			1680
Val Val Lys Gly Pro Gly His Thr Gly Gly Asp Leu Leu Gln Tyr Asn			
	545	550	555
aga agt act ggt tct gta gga acc tta ttt cta gct cga tat ggc cta			1728
Arg Ser Thr Gly Ser Val Gly Thr Leu Phe Leu Ala Arg Tyr Gly Leu			
	565	570	575
gca tta gaa aaa gca ggg aaa tat cgt gta aga ctg aga tat gct act			1776
Ala Leu Glu Lys Ala Gly Lys Tyr Arg Val Arg Leu Arg Tyr Ala Thr			
	580	585	590
gat gca gat att gta ttg cat gta aac gat gct cag att cag atg cca			1824
Asp Ala Asp Ile Val Leu His Val Asn Asp Ala Gln Ile Gln Met Pro			
	595	600	605
aaa aca atg aac cca ggt gag gat ctg aca tct aaa act ttt aaa gtt			1872
Lys Thr Met Asn Pro Gly Glu Asp Leu Thr Ser Lys Thr Phe Lys Val			
	610	615	620
gca gat gct atc aca aca gtt aat tta gca aca gat agt tcg gtt gca			1920
Ala Asp Ala Ile Thr Thr Val Asn Leu Ala Thr Asp Ser Ser Val Ala			
	625	630	635
gtt aaa cat aat gta ggt gaa gac cct aat tca aca tta tct ggt ata			1968
Val Lys His Asn Val Gly Glu Asp Pro Asn Ser Thr Leu Ser Gly Ile			
	645	650	655
gtt tac gtt gac cga atc gaa ttc atc cca gta gat gag aca tat gaa			2016
Val Tyr Val Asp Arg Ile Glu Phe Ile Pro Val Asp Glu Thr Tyr Glu			
	660	665	670

gcg gaa
Ala Glu

2022

<210> 50
<211> 674
<212> PRT
<213> *Bacillus thuringiensis* (mutated)

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Pro Thr Asn Ala Leu Gln Asn Met Asp Tyr Lys Asp Tyr Leu Lys Met
35 40 45
Ser Ala Gly Asn Ala Ser Glu Tyr Pro Gly Ser Pro Glu Val Leu Val
50 55 60
Ser Gly Gln Asp Ala Ala Lys Ala Ala Ile Asp Ile Val Gly Lys Leu
65 70 75 80
Leu Ser Gly Leu Gly Val Pro Phe Val Gly Pro Ile Val Ser Leu Tyr
85 90 95
Thr Gln Leu Ile Asp Ile Leu Trp Pro Ser Gly Glu Lys Ser Gln Trp
100 105 110
Glu Ile Phe Met Glu Gln Val Glu Glu Leu Ile Asn Gln Lys Ile Ala
115 120 125
Glu Tyr Ala Arg Asn Lys Ala Leu Ser Glu Leu Glu Gly Leu Gly Asn
130 135 140
Asn Tyr Gln Leu Tyr Leu Thr Ala Leu Glu Glu Trp Glu Glu Asn Pro
145 150 155 160
Asn Gly Ser Arg Phe Arg Ser Arg Gln Ala Leu Arg Asp Val Arg Asn
165 170 175
Arg Phe Glu Ile Leu Asp Ser Leu Phe Thr Gln Tyr Met Pro Ser Phe
180 185 190
Arg Val Thr Asn Phe Glu Val Pro Phe Leu Thr Val Tyr Ala Met Ala
195 200 205
Ala Asn Leu His Leu Leu Leu Leu Lys Asp Ala Ser Ile Phe Gly Glu
210 215 220
Glu Trp Gly Trp Ser Thr Thr Thr Ile Asn Asn Tyr Tyr Asp Arg Gln
225 230 235 240
Met Lys Leu Thr Ala Glu Tyr Ser Asp His Cys Val Lys Trp Tyr Glu
245 250 255
Thr Gly Leu Ala Lys Leu Lys Gly Thr Ser Ala Lys Gln Trp Val Asp
260 265 270
Tyr Asn Gln Phe Arg Arg Glu Met Thr Leu Ala Val Leu Asp Val Val
275 280 285
Ala Leu Phe Pro Asn Tyr Asp Thr Arg Thr Tyr Pro Met Glu Thr Lys
290 295 300
Ala Gln Leu Thr Arg Glu Val Tyr Thr Asp Pro Leu Gly Ala Val Asn
305 310 315 320
Val Ser Ser Ile Gly Ser Trp Tyr Asp Lys Ala Pro Ser Phe Gly Val
325 330 335
Ile Glu Ser Ser Val Ile Arg Pro Pro His Val Phe Asp Tyr Ile Thr
340 345 350
Gly Leu Thr Val Tyr Thr Gln Ser Arg Ser Ile Ser Ser Ala Arg Tyr


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      355              360              365
Ile Arg His Trp Ala Gly His Gln Ile Ser Tyr His Arg Val Ser Arg
      370              375              380
Gly Ser Asn Leu Gln Gln Met Tyr Gly Thr Asn Gln Asn Leu His Ser
385              390              395              400
Thr Ser Thr Phe Asp Phe Thr Asn Tyr Asp Ile Tyr Lys Thr Leu Ser
      405              410              415
Lys Asp Ala Val Leu Leu Asp Ile Val Tyr Pro Gly Tyr Thr Tyr Ile
      420              425              430
Phe Phe Gly Met Pro Glu Val Glu Phe Phe Met Val Asn Gln Leu Asn
      435              440              445
Asn Thr Arg Lys Thr Leu Lys Tyr Asn Pro Val Ser Lys Asp Ile Ile
      450              455              460
Ala Ser Thr Arg Asp Ser Glu Leu Glu Leu Pro Pro Glu Thr Ser Asp
465              470              475              480
Gln Pro Asn Tyr Glu Ser Tyr Ser His Arg Leu Cys His Ile Thr Ser
      485              490              495
Ile Pro Ala Thr Gly Asn Thr Thr Gly Leu Val Pro Val Phe Ser Trp
      500              505              510
Thr His Arg Ser Ala Asp Leu Asn Asn Thr Ile Tyr Ser Asp Lys Ile
      515              520              525
Thr Gln Ile Pro Ala Val Lys Cys Trp Asp Asn Leu Pro Phe Val Pro
      530              535              540
Val Val Lys Gly Pro Gly His Thr Gly Gly Asp Leu Leu Gln Tyr Asn
545              550              555              560
Arg Ser Thr Gly Ser Val Gly Thr Leu Phe Leu Ala Arg Tyr Gly Leu
      565              570              575
Ala Leu Glu Lys Ala Gly Lys Tyr Arg Val Arg Leu Arg Tyr Ala Thr
      580              585              590
Asp Ala Asp Ile Val Leu His Val Asn Asp Ala Gln Ile Gln Met Pro
      595              600              605
Lys Thr Met Asn Pro Gly Glu Asp Leu Thr Ser Lys Thr Phe Lys Val
      610              615              620
Ala Asp Ala Ile Thr Thr Val Asn Leu Ala Thr Asp Ser Ser Val Ala
625              630              635              640
Val Lys His Asn Val Gly Glu Asp Pro Asn Ser Thr Leu Ser Gly Ile
      645              650              655
Val Tyr Val Asp Arg Ile Glu Phe Ile Pro Val Asp Glu Thr Tyr Glu
      660              665              670
Ala Glu

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<210> 51
<211> 2031
<212> DNA
<213> Bacillus thuringiensis (mutated)

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<220>
<221> CDS
<222> (1)...(2031)

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tct act tct gta tcc aat gat tct aac aga tac cct ttt gcg aat gag	96
Ser Thr Ser Val Ser Asn Asp Ser Asn Arg Tyr Pro Phe Ala Asn Glu	
20 25 30	
cca aca aat gcg cta caa aat atg gat tat aaa gat tat tta aaa atg	144
Pro Thr Asn Ala Leu Gln Asn Met Asp Tyr Lys Asp Tyr Leu Lys Met	
35 40 45	
tct gcg gga aat gct agt gaa tac cct ggt tca cct gaa gta ctt gtt	192
Ser Ala Gly Asn Ala Ser Glu Tyr Pro Gly Ser Pro Glu Val Leu Val	
50 55 60	
agc gga caa gat gca gct aag gcc gca att gat ata gta ggt aaa tta	240
Ser Gly Gln Asp Ala Ala Lys Ala Ala Ile Asp Ile Val Gly Lys Leu	
65 70 75 80	
cta tca ggt tta ggg gtc cca ttt gtt ggg ccg ata gtg agt ctt tat	288
Leu Ser Gly Leu Gly Val Pro Phe Val Gly Pro Ile Val Ser Leu Tyr	
85 90 95	
act caa ctt att gat att ctg tgg cct tca ggg gaa aag agt caa tgg	336
Thr Gln Leu Ile Asp Ile Leu Trp Pro Ser Gly Glu Lys Ser Gln Trp	
100 105 110	
gaa att ttt atg gaa caa gta gaa gaa ctc att aat caa aaa ata gca	384
Glu Ile Phe Met Glu Gln Val Glu Glu Leu Ile Asn Gln Lys Ile Ala	
115 120 125	
gaa tat gca agg aat aaa gcg ctt tcg gaa tta gaa gga tta ggt aat	432
Glu Tyr Ala Arg Asn Lys Ala Leu Ser Glu Leu Glu Gly Leu Gly Asn	
130 135 140	
aat tac caa tta tat cta act gcg ctt gaa gaa tgg gaa gaa aat cca	480
Asn Tyr Gln Leu Tyr Leu Thr Ala Leu Glu Glu Trp Glu Glu Asn Pro	
145 150 155 160	
ttt cga agt cga ggt agt tta aat ggt tcc cgg cca gcc tta cga gat	528
Phe Arg Ser Arg Gly Ser Leu Asn Gly Ser Arg Pro Ala Leu Arg Asp	
165 170 175	
gtg cga aat cga ttt gaa atc ctg gat agt tta ttt acg caa tat atg	576
Val Arg Asn Arg Phe Glu Ile Leu Asp Ser Leu Phe Thr Gln Tyr Met	
180 185 190	
cca tct ttt aga gtg aca aat ttt gaa gta cca ttc ctt act gta tat	624
Pro Ser Phe Arg Val Thr Asn Phe Glu Val Pro Phe Leu Thr Val Tyr	
195 200 205	
gca atg gca gcc aac ctt cat tta ctg tta tta aag gac gcg tca att	672
Ala Met Ala Ala Asn Leu His Leu Leu Leu Leu Lys Asp Ala Ser Ile	
210 215 220	
ttt gga gaa gaa tgg gga tgg tca aca act act att aat aac tat tat	720
Phe Gly Glu Glu Trp Gly Trp Ser Thr Thr Thr Ile Asn Asn Tyr Tyr	
225 230 235 240	
gat cgt caa atg aaa ctt act gca gaa tat tct gat cac tgt gta aag	768

Asp	Arg	Gln	Met	Lys	Leu	Thr	Ala	Glu	Tyr	Ser	Asp	His	Cys	Val	Lys	
				245					250					255		
tgg	tat	gaa	act	ggg	tta	gca	aaa	tta	aaa	ggc	acg	agc	gct	aaa	caa	816
Trp	Tyr	Glu	Thr	Gly	Leu	Ala	Lys	Leu	Lys	Gly	Thr	Ser	Ala	Lys	Gln	
			260					265					270			
tgg	gtt	gac	tat	aac	caa	ttc	cgt	aga	gaa	atg	aca	ctg	gcg	gtt	tta	864
Trp	Val	Asp	Tyr	Asn	Gln	Phe	Arg	Arg	Glu	Met	Thr	Leu	Ala	Val	Leu	
		275					280					285				
gat	gtt	gtt	gca	tta	ttc	cca	aat	tat	gac	aca	cgc	acg	tac	cca	atg	912
Asp	Val	Val	Ala	Leu	Phe	Pro	Asn	Tyr	Asp	Thr	Arg	Thr	Tyr	Pro	Met	
	290					295				300						
gaa	acg	aaa	gca	caa	cta	aca	agg	gaa	gta	tat	aca	gat	cca	ctg	ggc	960
Glu	Thr	Lys	Ala	Gln	Leu	Thr	Arg	Glu	Val	Tyr	Thr	Asp	Pro	Leu	Gly	
305				310					315					320		
gcg	gta	aac	gtg	tct	tca	att	ggg	tcc	tgg	tat	gac	aaa	gca	cct	tct	1008
Ala	Val	Asn	Val	Ser	Ser	Ile	Gly	Ser	Trp	Tyr	Asp	Lys	Ala	Pro	Ser	
			325					330						335		
ttc	gga	gtg	ata	gaa	tca	tcc	gtt	att	cga	cca	ccc	cat	gta	ttt	gat	1056
Phe	Gly	Val	Ile	Glu	Ser	Ser	Val	Ile	Arg	Pro	Pro	His	Val	Phe	Asp	
		340					345						350			
tat	ata	acg	gga	ctc	aca	gtg	tat	aca	caa	tca	aga	agc	att	tct	tcc	1104
Tyr	Ile	Thr	Gly	Leu	Thr	Val	Tyr	Thr	Gln	Ser	Arg	Ser	Ile	Ser	Ser	
	355					360					365					
gct	cgc	tat	ata	aga	cat	tgg	gct	ggg	cat	caa	ata	agc	tac	cat	cgt	1152
Ala	Arg	Tyr	Ile	Arg	His	Trp	Ala	Gly	His	Gln	Ile	Ser	Tyr	His	Arg	
	370				375					380						
gtc	agt	agg	ggg	agt	aat	ctt	caa	caa	atg	tat	gga	act	aat	caa	aat	1200
Val	Ser	Arg	Gly	Ser	Asn	Leu	Gln	Gln	Met	Tyr	Gly	Thr	Asn	Gln	Asn	
385				390					395					400		
cta	cac	agc	act	agt	acc	ttt	gat	ttt	acg	aat	tat	gat	att	tac	aag	1248
Leu	His	Ser	Thr	Ser	Thr	Phe	Asp	Phe	Thr	Asn	Tyr	Asp	Ile	Tyr	Lys	
			405					410						415		
act	cta	tca	aag	gat	gca	gta	ctc	ctt	gat	att	gtt	tac	cct	ggg	tat	1296
Thr	Leu	Ser	Lys	Asp	Ala	Val	Leu	Leu	Asp	Ile	Val	Tyr	Pro	Gly	Tyr	
			420				425						430			
acg	tat	ata	ttt	ttt	gga	atg	cca	gaa	gtc	gag	ttt	ttc	atg	gta	aac	1344
Thr	Tyr	Ile	Phe	Phe	Gly	Met	Pro	Glu	Val	Glu	Phe	Phe	Met	Val	Asn	
	435					440					445					
caa	ttg	aat	aat	acc	aga	aag	acg	tta	aag	tat	aat	cca	gtt	tcc	aaa	1392
Gln	Leu	Asn	Asn	Thr	Arg	Lys	Thr	Leu	Lys	Tyr	Asn	Pro	Val	Ser	Lys	
	450					455				460						
gat	att	ata	gcg	agt	aca	aga	gat	tcg	gaa	tta	gaa	tta	cct	cca	gaa	1440
Asp	Ile	Ile	Ala	Ser	Thr	Arg	Asp	Ser	Glu	Leu	Glu	Leu	Pro	Pro	Glu	

465	470	475	480	
act tca gat caa cca aat tat gag tca tat agc cat aga tta tgt cat				1488
Thr Ser Asp Gln Pro Asn Tyr Glu Ser Tyr Ser His Arg Leu Cys His				
	485	490	495	
atc aca agt att ccc gcg acg ggt aac act acc gga tta gta cct gta				1536
Ile Thr Ser Ile Pro Ala Thr Gly Asn Thr Thr Gly Leu Val Pro Val				
	500	505	510	
ttt tct tgg aca cat cga agt gca gat tta aac aat aca ata tat tca				1584
Phe Ser Trp Thr His Arg Ser Ala Asp Leu Asn Asn Thr Ile Tyr Ser				
	515	520	525	
gat aaa atc act caa att ccg gcc gtt aaa tgt tgg gat aat tta ccg				1632
Asp Lys Ile Thr Gln Ile Pro Ala Val Lys Cys Trp Asp Asn Leu Pro				
	530	535	540	
ttt gtt cca gtg gta aaa gga cca gga cat aca gga ggg gat tta tta				1680
Phe Val Pro Val Val Lys Gly Pro Gly His Thr Gly Gly Asp Leu Leu				
	545	550	555	560
cag tat aat aga agt act ggt tct gta gga acc tta ttt cta gct cga				1728
Gln Tyr Asn Arg Ser Thr Gly Ser Val Gly Thr Leu Phe Leu Ala Arg				
	565	570	575	
tat ggc cta gca tta gaa aaa gca ggg aaa tat cgt gta aga ctg aga				1776
Tyr Gly Leu Ala Leu Glu Lys Ala Gly Lys Tyr Arg Val Arg Leu Arg				
	580	585	590	
tat gct act gat gca gat att gta ttg cat gta aac gat gct cag att				1824
Tyr Ala Thr Asp Ala Asp Ile Val Leu His Val Asn Asp Ala Gln Ile				
	595	600	605	
cag atg cca aaa aca atg aac cca ggt gag gat ctg aca tct aaa act				1872
Gln Met Pro Lys Thr Met Asn Pro Gly Glu Asp Leu Thr Ser Lys Thr				
	610	615	620	
ttt aaa gtt gca gat gct atc aca aca gtt aat tta gca aca gat agt				1920
Phe Lys Val Ala Asp Ala Ile Thr Thr Val Asn Leu Ala Thr Asp Ser				
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tcg gtt gca gtt aaa cat aat gta ggt gaa gac cct aat tca aca tta				1968
Ser Val Ala Val Lys His Asn Val Gly Glu Asp Pro Asn Ser Thr Leu				
	645	650	655	
tct ggt ata gtt tac gtt gac cga atc gaa ttc atc cca gta gat gag				2016
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aca tat gaa gcg gaa				2031
Thr Tyr Glu Ala Glu				
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<210> 52
<211> 677

<212> PRT

<213> *Bacillus thuringiensis* (mutated)

<400> 52

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			20					25					30		
Pro	Thr	Asn	Ala	Leu	Gln	Asn	Met	Asp	Tyr	Lys	Asp	Tyr	Leu	Lys	Met
		35					40					45			
Ser	Ala	Gly	Asn	Ala	Ser	Glu	Tyr	Pro	Gly	Ser	Pro	Glu	Val	Leu	Val
	50					55					60				
Ser	Gly	Gln	Asp	Ala	Ala	Lys	Ala	Ala	Ile	Asp	Ile	Val	Gly	Lys	Leu
65				70						75					80
Leu	Ser	Gly	Leu	Gly	Val	Pro	Phe	Val	Gly	Pro	Ile	Val	Ser	Leu	Tyr
			85						90					95	
Thr	Gln	Leu	Ile	Asp	Ile	Leu	Trp	Pro	Ser	Gly	Glu	Lys	Ser	Gln	Trp
		100						105					110		
Glu	Ile	Phe	Met	Glu	Gln	Val	Glu	Glu	Leu	Ile	Asn	Gln	Lys	Ile	Ala
		115					120					125			
Glu	Tyr	Ala	Arg	Asn	Lys	Ala	Leu	Ser	Glu	Leu	Glu	Gly	Leu	Gly	Asn
	130					135						140			
Asn	Tyr	Gln	Leu	Tyr	Leu	Thr	Ala	Leu	Glu	Glu	Trp	Glu	Glu	Asn	Pro
145				150						155					160
Phe	Arg	Ser	Arg	Gly	Ser	Leu	Asn	Gly	Ser	Arg	Pro	Ala	Leu	Arg	Asp
			165						170					175	
Val	Arg	Asn	Arg	Phe	Glu	Ile	Leu	Asp	Ser	Leu	Phe	Thr	Gln	Tyr	Met
		180						185					190		
Pro	Ser	Phe	Arg	Val	Thr	Asn	Phe	Glu	Val	Pro	Phe	Leu	Thr	Val	Tyr
	195						200					205			
Ala	Met	Ala	Ala	Asn	Leu	His	Leu	Leu	Leu	Leu	Lys	Asp	Ala	Ser	Ile
	210					215						220			
Phe	Gly	Glu	Glu	Trp	Gly	Trp	Ser	Thr	Thr	Thr	Ile	Asn	Asn	Tyr	Tyr
225				230						235					240
Asp	Arg	Gln	Met	Lys	Leu	Thr	Ala	Glu	Tyr	Ser	Asp	His	Cys	Val	Lys
			245						250					255	
Trp	Tyr	Glu	Thr	Gly	Leu	Ala	Lys	Leu	Lys	Gly	Thr	Ser	Ala	Lys	Gln
		260						265					270		
Trp	Val	Asp	Tyr	Asn	Gln	Phe	Arg	Arg	Glu	Met	Thr	Leu	Ala	Val	Leu
		275					280					285			
Asp	Val	Val	Ala	Leu	Phe	Pro	Asn	Tyr	Asp	Thr	Arg	Thr	Tyr	Pro	Met
	290					295					300				
Glu	Thr	Lys	Ala	Gln	Leu	Thr	Arg	Glu	Val	Tyr	Thr	Asp	Pro	Leu	Gly
305				310						315					320
Ala	Val	Asn	Val	Ser	Ser	Ile	Gly	Ser	Trp	Tyr	Asp	Lys	Ala	Pro	Ser
			325						330					335	
Phe	Gly	Val	Ile	Glu	Ser	Ser	Val	Ile	Arg	Pro	Pro	His	Val	Phe	Asp
		340						345					350		
Tyr	Ile	Thr	Gly	Leu	Thr	Val	Tyr	Thr	Gln	Ser	Arg	Ser	Ile	Ser	Ser
	355						360					365			
Ala	Arg	Tyr	Ile	Arg	His	Trp	Ala	Gly	His	Gln	Ile	Ser	Tyr	His	Arg
	370					375					380				
Val	Ser	Arg	Gly	Ser	Asn	Leu	Gln	Gln	Met	Tyr	Gly	Thr	Asn	Gln	Asn
385				390						395					400
Leu	His	Ser	Thr	Ser	Thr	Phe	Asp	Phe	Thr	Asn	Tyr	Asp	Ile	Tyr	Lys
			405						410				415		
Thr	Leu	Ser	Lys	Asp	Ala	Val	Leu	Leu	Asp	Ile	Val	Tyr	Pro	Gly	Tyr

tct gcg gga aat gct agt gaa tac cct ggt tca cct gaa gta ctt gtt	192
Ser Ala Gly Asn Ala Ser Glu Tyr Pro Gly Ser Pro Glu Val Leu Val	
50 55 60	
agc gga caa gat gca gct aag gcc gca att gat ata gta ggt aaa tta	240
Ser Gly Gln Asp Ala Ala Lys Ala Ala Ile Asp Ile Val Gly Lys Leu	
65 70 75 80	
cta tca ggt tta ggg gtc cca ttt gtt ggg ccg ata gtg agt ctt tat	288
Leu Ser Gly Leu Gly Val Pro Phe Val Gly Pro Ile Val Ser Leu Tyr	
85 90 95	
act caa ctt att gat att ctg tgg cct tca ggg gaa aag agt caa tgg	336
Thr Gln Leu Ile Asp Ile Leu Trp Pro Ser Gly Glu Lys Ser Gln Trp	
100 105 110	
gaa att ttt atg gaa caa gta gaa gaa ctc att aat caa aaa ata gca	384
Glu Ile Phe Met Glu Gln Val Glu Glu Leu Ile Asn Gln Lys Ile Ala	
115 120 125	
gaa tat gca agg aat aaa gcg ctt tcg gaa tta gaa gga tta ggt aat	432
Glu Tyr Ala Arg Asn Lys Ala Leu Ser Glu Leu Glu Gly Leu Gly Asn	
130 135 140	
aat tac caa tta tat cta act gcg ctt gaa gaa tgg gaa gaa aat cca	480
Asn Tyr Gln Leu Tyr Leu Thr Ala Leu Glu Glu Trp Glu Glu Asn Pro	
145 150 155 160	
ttt cga cga ggt ttt cga cga ggt gcc tta cga gat gtg cga aat cga	528
Phe Arg Arg Gly Phe Arg Arg Gly Ala Leu Arg Asp Val Arg Asn Arg	
165 170 175	
ttt gaa atc ctg gat agt tta ttt acg caa tat atg cca tct ttt aga	576
Phe Glu Ile Leu Asp Ser Leu Phe Thr Gln Tyr Met Pro Ser Phe Arg	
180 185 190	
gtg aca aat ttt gaa gta cca ttc ctt act gta tat gca atg gca gcc	624
Val Thr Asn Phe Glu Val Pro Phe Leu Thr Val Tyr Ala Met Ala Ala	
195 200 205	
aac ctt cat tta ctg tta tta aag gac gcg tca att ttt gga gaa gaa	672
Asn Leu His Leu Leu Leu Leu Lys Asp Ala Ser Ile Phe Gly Glu Glu	
210 215 220	
tgg gga tgg tca aca act act att aat aac gtg gtg gat cgt caa atg	720
Trp Gly Trp Ser Thr Thr Thr Ile Asn Asn Val Val Asp Arg Gln Met	
225 230 235 240	
aaa ctt act gca gaa tat tct gat cac tgt gta aag tgg tat gaa act	768
Lys Leu Thr Ala Glu Tyr Ser Asp His Cys Val Lys Trp Tyr Glu Thr	
245 250 255	
ggg tta gca aaa tta aaa ggc acg agc gct aaa caa tgg gtt gac tat	816
Gly Leu Ala Lys Leu Lys Gly Thr Ser Ala Lys Gln Trp Val Asp Tyr	
260 265 270	
aac caa ttc cgt aga gaa atg aca ctg gcg gtt tta gat gtt gtt gca	864

Asn Gln Phe Arg Arg Glu Met Thr Leu Ala Val Leu Asp Val Val Ala	
275 280 285	
tta ttc cca aat tat gac aca ata acg tac cca ata gaa acg aaa gca	912
Leu Phe Pro Asn Tyr Asp Thr Ile Thr Tyr Pro Ile Glu Thr Lys Ala	
290 295 300	
caa cta aca agg gaa gta tat aca gat cca ctg ggc gcg gta aac gtg	960
Gln Leu Thr Arg Glu Val Tyr Thr Asp Pro Leu Gly Ala Val Asn Val	
305 310 315 320	
tct tca att ggt tcc tgg tat gac aaa gca cct tct ttc gga gtg ata	1008
Ser Ser Ile Gly Ser Trp Tyr Asp Lys Ala Pro Ser Phe Gly Val Ile	
325 330 335	
gaa tca tcc gtt att cga cca ccc cat gta ttt gat tat ata acg gga	1056
Glu Ser Ser Val Ile Arg Pro Pro His Val Phe Asp Tyr Ile Thr Gly	
340 345 350	
ctc aca gtg tat aca caa tca aga agc att tct tcc gct cgc tat ata	1104
Leu Thr Val Tyr Thr Gln Ser Arg Ser Ile Ser Ser Ala Arg Tyr Ile	
355 360 365	
aga cat tgg gct ggt cat caa ata agc tac cat cgt gtc agt agg ggt	1152
Arg His Trp Ala Gly His Gln Ile Ser Tyr His Arg Val Ser Arg Gly	
370 375 380	
agt aat ctt caa caa atg tat gga act aat caa aat cta cac agc act	1200
Ser Asn Leu Gln Gln Met Tyr Gly Thr Asn Gln Asn Leu His Ser Thr	
385 390 395 400	
agt acc ttt gat ttt acg aat tat gat att tac aag act cta tca aag	1248
Ser Thr Phe Asp Phe Thr Asn Tyr Asp Ile Tyr Lys Thr Leu Ser Lys	
405 410 415	
gat gca gta ctc ctt gat att gtt tac cct ggt tat acg tat ata ttt	1296
Asp Ala Val Leu Leu Asp Ile Val Tyr Pro Gly Tyr Thr Tyr Ile Phe	
420 425 430	
ttt gga atg cca gaa gtc gag ttt ttc atg gta aac caa ttg aat aat	1344
Phe Gly Met Pro Glu Val Glu Phe Phe Met Val Asn Gln Leu Asn Asn	
435 440 445	
acc aga aag acg tta aag tat aat cca gtt tcc aaa gat att ata gcg	1392
Thr Arg Lys Thr Leu Lys Tyr Asn Pro Val Ser Lys Asp Ile Ile Ala	
450 455 460	
agt aca aga gat tcg gaa tta gaa tta cct cca gaa act tca gat caa	1440
Ser Thr Arg Asp Ser Glu Leu Glu Leu Pro Pro Glu Thr Ser Asp Gln	
465 470 475 480	
cca aat tat gag tca tat agc cat aga tta tgt cat atc aca agt att	1488
Pro Asn Tyr Glu Ser Tyr Ser His Arg Leu Cys His Ile Thr Ser Ile	
485 490 495	
ccc gcg acg ggt aac act acc gga tta gta cct gta ttt tct tgg aca	1536
Pro Ala Thr Gly Asn Thr Thr Gly Leu Val Pro Val Phe Ser Trp Thr	

500	505	510	
cat cga agt gca gat tta aac aat aca ata tat tca gat aaa atc act			1584
His Arg Ser Ala Asp Leu Asn Asn Thr Ile Tyr Ser Asp Lys Ile Thr			
515	520	525	
caa att ccg gcc gtt aaa tgt tgg gat aat tta ccg ttt gtt cca gtg			1632
Gln Ile Pro Ala Val Lys Cys Trp Asp Asn Leu Pro Phe Val Pro Val			
530	535	540	
gta aaa gga cca gga cat aca gga ggg gat tta tta cag tat aat aga			1680
Val Lys Gly Pro Gly His Thr Gly Gly Asp Leu Leu Gln Tyr Asn Arg			
545	550	555	560
agt act ggt tct gta gga acc tta ttt cta gct cga tat ggc cta gca			1728
Ser Thr Gly Ser Val Gly Thr Leu Phe Leu Ala Arg Tyr Gly Leu Ala			
565	570	575	
tta gaa aaa gca ggg aaa tat cgt gta aga ctg aga tat gct act gat			1776
Leu Glu Lys Ala Gly Lys Tyr Arg Val Arg Leu Arg Tyr Ala Thr Asp			
580	585	590	
gca gat att gta ttg cat gta aac gat gct cag att cag atg cca aaa			1824
Ala Asp Ile Val Leu His Val Asn Asp Ala Gln Ile Gln Met Pro Lys			
595	600	605	
aca atg aac cca ggt gag gat ctg aca tct aaa act ttt aaa gtt gca			1872
Thr Met Asn Pro Gly Glu Asp Leu Thr Ser Lys Thr Phe Lys Val Ala			
610	615	620	
gat gct atc aca aca gtt aat tta gca aca gat agt tcg gtt gca gtt			1920
Asp Ala Ile Thr Thr Val Asn Leu Ala Thr Asp Ser Ser Val Ala Val			
625	630	635	640
aaa cat aat gta ggt gaa gac cct aat tca aca tta tct ggt ata gtt			1968
Lys His Asn Val Gly Glu Asp Pro Asn Ser Thr Leu Ser Gly Ile Val			
645	650	655	
tac gtt gac cga atc gaa ttc atc cca gta gat gag aca tat gaa gcg			2016
Tyr Val Asp Arg Ile Glu Phe Ile Pro Val Asp Glu Thr Tyr Glu Ala			
660	665	670	
gaa			2019
Glu			

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 <212> PRT
 <213> Bacillus thuringiensis (mutated)

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 20 25 30

RTA01/2138018v1

485 490 495
 Pro Ala Thr Gly Asn Thr Thr Gly Leu Val Pro Val Phe Ser Trp Thr
 500 505 510
 His Arg Ser Ala Asp Leu Asn Asn Thr Ile Tyr Ser Asp Lys Ile Thr
 515 520 525
 Gln Ile Pro Ala Val Lys Cys Trp Asp Asn Leu Pro Phe Val Pro Val
 530 535 540
 Val Lys Gly Pro Gly His Thr Gly Gly Asp Leu Leu Gln Tyr Asn Arg
 545 550 555 560
 Ser Thr Gly Ser Val Gly Thr Leu Phe Leu Ala Arg Tyr Gly Leu Ala
 565 570 575
 Leu Glu Lys Ala Gly Lys Tyr Arg Val Arg Leu Arg Tyr Ala Thr Asp
 580 585 590
 Ala Asp Ile Val Leu His Val Asn Asp Ala Gln Ile Gln Met Pro Lys
 595 600 605
 Thr Met Asn Pro Gly Glu Asp Leu Thr Ser Lys Thr Phe Lys Val Ala
 610 615 620
 Asp Ala Ile Thr Thr Val Asn Leu Ala Thr Asp Ser Ser Val Ala Val
 625 630 635 640
 Lys His Asn Val Gly Glu Asp Pro Asn Ser Thr Leu Ser Gly Ile Val
 645 650 655
 Tyr Val Asp Arg Ile Glu Phe Ile Pro Val Asp Glu Thr Tyr Glu Ala
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 Glu

<210> 55
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 <212> DNA
 <213> *Bacillus thuringiensis* (mutated)

<220>
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 <222> (1)...(2019)

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 tct act tct gta tcc aat gat tct aac aga tac cct ttt gcg aat gag 96
 Ser Thr Ser Val Ser Asn Asp Ser Asn Arg Tyr Pro Phe Ala Asn Glu
 20 25 30
 cca aca aat gcg cta caa aat atg gat tat aaa gat tat gca gta ggg 144
 Pro Thr Asn Ala Leu Gln Asn Met Asp Tyr Lys Asp Tyr Ala Val Gly
 35 40 45
 tct gcg gga aat gct agt gaa tac cct ggt tca cct gaa gta ctt gtt 192
 Ser Ala Gly Asn Ala Ser Glu Tyr Pro Gly Ser Pro Glu Val Leu Val
 50 55 60
 agc gga caa gat gca gct aag gcc gca att gat ata gta ggt aaa tta 240
 Ser Gly Gln Asp Ala Ala Lys Ala Ala Ile Asp Ile Val Gly Lys Leu
 65 70 75 80

cta tca ggt tta ggg gtc cca ttt gtt ggg ccg ata gtg agt ctt tat	288
Leu Ser Gly Leu Gly Val Pro Phe Val Gly Pro Ile Val Ser Leu Tyr	
85 90 95	
act caa ctt att gat att ctg tgg cct tca ggg gaa aag agt caa tgg	336
Thr Gln Leu Ile Asp Ile Leu Trp Pro Ser Gly Glu Lys Ser Gln Trp	
100 105 110	
gaa att ttt atg gaa caa gta gaa gaa ctc att aat caa aaa ata gca	384
Glu Ile Phe Met Glu Gln Val Glu Glu Leu Ile Asn Gln Lys Ile Ala	
115 120 125	
gaa tat gca agg aat aaa gcg ctt tcg gaa tta gaa gga tta ggt aat	432
Glu Tyr Ala Arg Asn Lys Ala Leu Ser Glu Leu Glu Gly Leu Gly Asn	
130 135 140	
aat tac caa tta tat cta act gcg ctt gaa gaa tgg gaa gaa aat cca	480
Asn Tyr Gln Leu Tyr Leu Thr Ala Leu Glu Glu Trp Glu Glu Asn Pro	
145 150 155 160	
ttt cga cga ggt ttt cga cga ggt gcc tta cga gat gtg cga aat cga	528
Phe Arg Arg Gly Phe Arg Arg Gly Ala Leu Arg Asp Val Arg Asn Arg	
165 170 175	
ttt gaa atc ctg gat agt tta ttt acg caa tat atg cca tct ttt aga	576
Phe Glu Ile Leu Asp Ser Leu Phe Thr Gln Tyr Met Pro Ser Phe Arg	
180 185 190	
gtg aca aat ttt gaa gta cca ttc ctt act gta tat gca atg gca gcc	624
Val Thr Asn Phe Glu Val Pro Phe Leu Thr Val Tyr Ala Met Ala Ala	
195 200 205	
aac ctt cat tta ctg tta tta aag gac gcg tca att ttt gga gaa gaa	672
Asn Leu His Leu Leu Leu Leu Lys Asp Ala Ser Ile Phe Gly Glu Glu	
210 215 220	
tgg gga tgg tca aca act act att aat aac tat tat gat cgt caa atg	720
Trp Gly Trp Ser Thr Thr Thr Ile Asn Asn Tyr Tyr Asp Arg Gln Met	
225 230 235 240	
aaa ctt act gca gaa tat tct gat cac tgt gta aag tgg tat gaa act	768
Lys Leu Thr Ala Glu Tyr Ser Asp His Cys Val Lys Trp Tyr Glu Thr	
245 250 255	
ggg tta gca aaa tta aaa ggc acg agc gct aaa caa tgg gtt gac tat	816
Gly Leu Ala Lys Leu Lys Gly Thr Ser Ala Lys Gln Trp Val Asp Tyr	
260 265 270	
aac caa ttc cgt aga gaa atg aca ctg gcg gtt tta gat gtt gtt gca	864
Asn Gln Phe Arg Arg Glu Met Thr Leu Ala Val Leu Asp Val Val Ala	
275 280 285	
tta ttc cca aat tat gac aca ata acg tac cca ata gaa acg aaa gca	912
Leu Phe Pro Asn Tyr Asp Thr Ile Thr Tyr Pro Ile Glu Thr Lys Ala	
290 295 300	
caa cta aca agg gaa gta tat aca gat cca ctg ggc gcg gta aac gtg	960

Gln Leu Thr Arg Glu Val Tyr Thr Asp Pro Leu Gly Ala Val Asn Val	
305 310 315 320	
tct tca att ggt tcc tgg tat gac aaa gca cct tct ttc gga gtg ata	1008
Ser Ser Ile Gly Ser Trp Tyr Asp Lys Ala Pro Ser Phe Gly Val Ile	
325 330 335	
gaa tca tcc gtt att cga cca ccc cat gta ttt gat tat ata acg gga	1056
Glu Ser Ser Val Ile Arg Pro Pro His Val Phe Asp Tyr Ile Thr Gly	
340 345 350	
ctc aca gtg tat aca caa tca aga agc att tct tcc gct cgc tat ata	1104
Leu Thr Val Tyr Thr Gln Ser Arg Ser Ile Ser Ser Ala Arg Tyr Ile	
355 360 365	
aga cat tgg gct ggt cat caa ata agc tac cat cgt gtc agt agg ggt	1152
Arg His Trp Ala Gly His Gln Ile Ser Tyr His Arg Val Ser Arg Gly	
370 375 380	
agt aat ctt caa caa atg tat gga act aat caa aat cta cac agc act	1200
Ser Asn Leu Gln Gln Met Tyr Gly Thr Asn Gln Asn Leu His Ser Thr	
385 390 395 400	
agt acc ttt gat ttt acg aat tat gat att tac aag act cta tca aag	1248
Ser Thr Phe Asp Phe Thr Asn Tyr Asp Ile Tyr Lys Thr Leu Ser Lys	
405 410 415	
gat gca gta ctc ctt gat att gtt tac cct ggt tat acg tat ata ttt	1296
Asp Ala Val Leu Leu Asp Ile Val Tyr Pro Gly Tyr Thr Tyr Ile Phe	
420 425 430	
ttt gga atg cca gaa gtc gag ttt ttc atg gta aac caa ttg aat aat	1344
Phe Gly Met Pro Glu Val Glu Phe Phe Met Val Asn Gln Leu Asn Asn	
435 440 445	
acc aga aag acg tta aag tat aat cca gtt tcc aaa gat att ata gcg	1392
Thr Arg Lys Thr Leu Lys Tyr Asn Pro Val Ser Lys Asp Ile Ile Ala	
450 455 460	
agt aca aga gat tcg gaa tta gaa tta cct cca gaa act tca gat caa	1440
Ser Thr Arg Asp Ser Glu Leu Glu Leu Pro Pro Glu Thr Ser Asp Gln	
465 470 475 480	
cca aat tat gag tca tat agc cat aga tta tgt cat atc aca agt att	1488
Pro Asn Tyr Glu Ser Tyr Ser His Arg Leu Cys His Ile Thr Ser Ile	
485 490 495	
ccc gcg acg ggt aac act acc gga tta gta cct gta ttt tct tgg aca	1536
Pro Ala Thr Gly Asn Thr Thr Gly Leu Val Pro Val Phe Ser Trp Thr	
500 505 510	
cat cga agt gca gat tta aac aat aca ata tat tca gat aaa atc act	1584
His Arg Ser Ala Asp Leu Asn Asn Thr Ile Tyr Ser Asp Lys Ile Thr	
515 520 525	
caa att ccg gcc gtt aaa tgt tgg gat aat tta ccg ttt gtt cca gtg	1632
Gln Ile Pro Ala Val Lys Cys Trp Asp Asn Leu Pro Phe Val Pro Val	

530	535	540	
gta aaa gga cca gga cat aca gga ggg gat tta tta cag tat aat aga			1680
Val Lys Gly Pro Gly His Thr Gly Gly Asp Leu Leu Gln Tyr Asn Arg			
545	550	555	560
agt act ggt tct gta gga acc tta ttt cta gct cga tat ggc cta gca			1728
Ser Thr Gly Ser Val Gly Thr Leu Phe Leu Ala Arg Tyr Gly Leu Ala			
565	570		575
tta gaa aaa gca ggg aaa tat cgt gta aga ctg aga tat gct act gat			1776
Leu Glu Lys Ala Gly Lys Tyr Arg Val Arg Leu Arg Tyr Ala Thr Asp			
580	585		590
gca gat att gta ttg cat gta aac gat gct cag att cag atg cca aaa			1824
Ala Asp Ile Val Leu His Val Asn Asp Ala Gln Ile Gln Met Pro Lys			
595	600		605
aca atg aac cca ggt gag gat ctg aca tct aaa act ttt aaa gtt gca			1872
Thr Met Asn Pro Gly Glu Asp Leu Thr Ser Lys Thr Phe Lys Val Ala			
610	615		620
gat gct atc aca aca gtt aat tta gca aca gat agt tcg gtt gca gtt			1920
Asp Ala Ile Thr Thr Val Asn Leu Ala Thr Asp Ser Ser Val Ala Val			
625	630	635	640
aaa cat aat gta ggt gaa gac cct aat tca aca tta tct ggt ata gtt			1968
Lys His Asn Val Gly Glu Asp Pro Asn Ser Thr Leu Ser Gly Ile Val			
645	650		655
tac gtt gac cga atc gaa ttc atc cca gta gat gag aca tat gaa gcg			2016
Tyr Val Asp Arg Ile Glu Phe Ile Pro Val Asp Glu Thr Tyr Glu Ala			
660	665		670
gaa			2019
Glu			

<210> 56
 <211> 673
 <212> PRT
 <213> *Bacillus thuringiensis* (mutated)

<400> 56
 Met Ser Pro Asn Asn Gln Asn Glu Tyr Glu Ile Ile Asp Ala Thr Pro
 1 5 10 15
 Ser Thr Ser Val Ser Asn Asp Ser Asn Arg Tyr Pro Phe Ala Asn Glu
 20 25 30
 Pro Thr Asn Ala Leu Gln Asn Met Asp Tyr Lys Asp Tyr Ala Val Gly
 35 40 45
 Ser Ala Gly Asn Ala Ser Glu Tyr Pro Gly Ser Pro Glu Val Leu Val
 50 55 60
 Ser Gly Gln Asp Ala Ala Lys Ala Ala Ile Asp Ile Val Gly Lys Leu
 65 70 75 80
 Leu Ser Gly Leu Gly Val Pro Phe Val Gly Pro Ile Val Ser Leu Tyr
 85 90 95

RTA01/2138018v1

545		550		555		560
Ser Thr Gly Ser Val Gly Thr Leu Phe Leu Ala Arg Tyr Gly Leu Ala						
	565		570		575	
Leu Glu Lys Ala Gly Lys Tyr Arg Val Arg Leu Arg Tyr Ala Thr Asp						
	580		585		590	
Ala Asp Ile Val Leu His Val Asn Asp Ala Gln Ile Gln Met Pro Lys						
	595		600		605	
Thr Met Asn Pro Gly Glu Asp Leu Thr Ser Lys Thr Phe Lys Val Ala						
	610		615		620	
Asp Ala Ile Thr Thr Val Asn Leu Ala Thr Asp Ser Ser Val Ala Val						
625		630		635		640
Lys His Asn Val Gly Glu Asp Pro Asn Ser Thr Leu Ser Gly Ile Val						
	645		650		655	
Tyr Val Asp Arg Ile Glu Phe Ile Pro Val Asp Glu Thr Tyr Glu Ala						
	660		665		670	
Glu						

<210> 57
 <211> 2019
 <212> DNA
 <213> Bacillus thuringiensis (mutated)

<220>
 <221> CDS
 <222> (1)...(2019)

<400> 57	
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Met Ser Pro Asn Asn Gln Asn Glu Tyr Glu Ile Ile Asp Ala Thr Pro	
1 5 10 15	
tct act tct gta tcc aat gat tct aac aga tac cct ttt gcg aat gag	96
Ser Thr Ser Val Ser Asn Asp Ser Asn Arg Tyr Pro Phe Ala Asn Glu	
20 25 30	
cca aca aat gcg cta caa aat atg gat tat aaa gat tat gca gta ggg	144
Pro Thr Asn Ala Leu Gln Asn Met Asp Tyr Lys Asp Tyr Ala Val Gly	
35 40 45	
tct gcg gga aat gct agt gaa tac cct ggt tca cct gaa gta ctt gtt	192
Ser Ala Gly Asn Ala Ser Glu Tyr Pro Gly Ser Pro Glu Val Leu Val	
50 55 60	
agc gga caa gat gca gct aag gcc gca att gat ata gta ggt aaa tta	240
Ser Gly Gln Asp Ala Ala Lys Ala Ala Ile Asp Ile Val Gly Lys Leu	
65 70 75 80	
cta tca ggt tta ggg gtc cca ttt gtt ggg ccg ata gtg agt ctt tat	288
Leu Ser Gly Leu Gly Val Pro Phe Val Gly Pro Ile Val Ser Leu Tyr	
85 90 95	
act caa ctt att gat att ctg tgg cct tca ggg gaa aag agt caa tgg	336
Thr Gln Leu Ile Asp Ile Leu Trp Pro Ser Gly Glu Lys Ser Gln Trp	
100 105 110	

gaa att ttt atg gaa caa gta gaa gaa ctc att aat caa aaa ata gca	384
Glu Ile Phe Met Glu Gln Val Glu Glu Leu Ile Asn Gln Lys Ile Ala	
115 120 125	
gaa tat gca agg aat aaa gcg ctt tcg gaa tta gaa gga tta ggt aat	432
Glu Tyr Ala Arg Asn Lys Ala Leu Ser Glu Leu Glu Gly Leu Gly Asn	
130 135 140	
aat tac caa tta tat cta act gcg ctt gaa gaa tgg gaa gaa aat cca	480
Asn Tyr Gln Leu Tyr Leu Thr Ala Leu Glu Glu Trp Glu Glu Asn Pro	
145 150 155 160	
ttt cga cga ggt ttt cga cga ggt gcc tta cga gat gtg cga aat cga	528
Phe Arg Arg Gly Phe Arg Arg Gly Ala Leu Arg Asp Val Arg Asn Arg	
165 170 175	
ttt gaa atc ctg gat agt tta ttt acg caa tat atg cca tct ttt aga	576
Phe Glu Ile Leu Asp Ser Leu Phe Thr Gln Tyr Met Pro Ser Phe Arg	
180 185 190	
gtg aca aat ttt gaa gta cca ttc ctt act gta tat gca atg gca gcc	624
Val Thr Asn Phe Glu Val Pro Phe Leu Thr Val Tyr Ala Met Ala Ala	
195 200 205	
aac ctt cat tta ctg tta tta aag gac gcg tca att ttt gga gaa gaa	672
Asn Leu His Leu Leu Leu Leu Lys Asp Ala Ser Ile Phe Gly Glu Glu	
210 215 220	
tgg gga tgg tca aca act act att aat aac tat tat gat cgt caa atg	720
Trp Gly Trp Ser Thr Thr Thr Ile Asn Asn Tyr Tyr Asp Arg Gln Met	
225 230 235 240	
aaa ctt act gca gaa tat tct gat cac tgt gta aag tgg tat gaa act	768
Lys Leu Thr Ala Glu Tyr Ser Asp His Cys Val Lys Trp Tyr Glu Thr	
245 250 255	
ggg tta gca aaa tta aaa ggc acg agc gct aaa caa tgg gtt gac tat	816
Gly Leu Ala Lys Leu Lys Gly Thr Ser Ala Lys Gln Trp Val Asp Tyr	
260 265 270	
aac caa ttc cgt aga gaa atg aca ctg gcg gtt tta gat gtt gtt gca	864
Asn Gln Phe Arg Arg Glu Met Thr Leu Ala Val Leu Asp Val Val Ala	
275 280 285	
tta ttc cca aat tat gac aca cgt acg tac cca atg gaa acg aaa gca	912
Leu Phe Pro Asn Tyr Asp Thr Arg Thr Tyr Pro Met Glu Thr Lys Ala	
290 295 300	
caa cta aca agg gaa gta tat aca gat cca ctg ggc gcg gta aac gtg	960
Gln Leu Thr Arg Glu Val Tyr Thr Asp Pro Leu Gly Ala Val Asn Val	
305 310 315 320	
tct tca att ggt tcc tgg tat gac aaa gca cct tct ttc gga gtg ata	1008
Ser Ser Ile Gly Ser Trp Tyr Asp Lys Ala Pro Ser Phe Gly Val Ile	
325 330 335	
gaa tca tcc gtt att cga cca ccc cat gta ttt gat tat ata acg gga	1056

Glu	Ser	Ser	Val	Ile	Arg	Pro	Pro	His	Val	Phe	Asp	Tyr	Ile	Thr	Gly		
			340					345					350				
ctc	aca	gtg	tat	aca	caa	tca	aga	agc	att	tct	tcc	gct	cgc	tat	ata	1104	
Leu	Thr	Val	Tyr	Thr	Gln	Ser	Arg	Ser	Ile	Ser	Ser	Ala	Arg	Tyr	Ile		
		355					360					365					
aga	cat	tgg	gct	ggg	cat	caa	ata	agc	tac	cat	cgt	gtc	agt	agg	ggg	1152	
Arg	His	Trp	Ala	Gly	His	Gln	Ile	Ser	Tyr	His	Arg	Val	Ser	Arg	Gly		
	370					375					380						
agt	aat	ctt	caa	caa	atg	tat	gga	act	aat	caa	aat	cta	cac	agc	act	1200	
Ser	Asn	Leu	Gln	Gln	Met	Tyr	Gly	Thr	Asn	Gln	Asn	Leu	His	Ser	Thr		
	385				390					395					400		
agt	acc	ttt	gat	ttt	acg	aat	tat	gat	att	tac	aag	act	cta	tca	aag	1248	
Ser	Thr	Phe	Asp	Phe	Thr	Asn	Tyr	Asp	Ile	Tyr	Lys	Thr	Leu	Ser	Lys		
				405					410						415		
gat	gca	gta	ctc	ctt	gat	att	gtt	tac	cct	ggg	tat	acg	tat	ata	ttt	1296	
Asp	Ala	Val	Leu	Leu	Asp	Ile	Val	Tyr	Pro	Gly	Tyr	Thr	Tyr	Ile	Phe		
			420					425						430			
ttt	gga	atg	cca	gaa	gtc	gag	ttt	ttc	atg	gta	aac	caa	ttg	aat	aat	1344	
Phe	Gly	Met	Pro	Glu	Val	Glu	Phe	Phe	Met	Val	Asn	Gln	Leu	Asn	Asn		
		435					440					445					
acc	aga	aag	acg	tta	aag	tat	aat	cca	gtt	tcc	aaa	gat	att	ata	gcg	1392	
Thr	Arg	Lys	Thr	Leu	Lys	Tyr	Asn	Pro	Val	Ser	Lys	Asp	Ile	Ile	Ala		
	450					455					460						
agt	aca	aga	gat	tcg	gaa	tta	gaa	tta	cct	cca	gaa	act	tca	gat	caa	1440	
Ser	Thr	Arg	Asp	Ser	Glu	Leu	Glu	Leu	Pro	Pro	Glu	Thr	Ser	Asp	Gln		
	465				470					475					480		
cca	aat	tat	gag	tca	tat	agc	cat	aga	tta	tgt	cat	atc	aca	agt	att	1488	
Pro	Asn	Tyr	Glu	Ser	Tyr	Ser	His	Arg	Leu	Cys	His	Ile	Thr	Ser	Ile		
				485					490						495		
ccc	gcg	acg	ggg	aac	act	acc	gga	tta	gta	cct	gta	ttt	tct	tgg	aca	1536	
Pro	Ala	Thr	Gly	Asn	Thr	Thr	Gly	Leu	Val	Pro	Val	Phe	Ser	Trp	Thr		
			500					505					510				
cat	cga	agt	gca	gat	tta	aac	aat	aca	ata	tat	tca	gat	aaa	atc	act	1584	
His	Arg	Ser	Ala	Asp	Leu	Asn	Asn	Thr	Ile	Tyr	Ser	Asp	Lys	Ile	Thr		
		515					520					525					
caa	att	ccg	gcc	gtt	aaa	tgt	tgg	gat	aat	tta	ccg	ttt	gtt	cca	gtg	1632	
Gln	Ile	Pro	Ala	Val	Lys	Cys	Trp	Asp	Asn	Leu	Pro	Phe	Val	Pro	Val		
	530					535					540						
gta	aaa	gga	cca	gga	cat	aca	gga	ggg	gat	tta	tta	cag	tat	aat	aga	1680	
Val	Lys	Gly	Pro	Gly	His	Thr	Gly	Gly	Asp	Leu	Leu	Gln	Tyr	Asn	Arg		
	545				550				555						560		
agt	act	ggg	tct	gta	gga	acc	tta	ttt	cta	gct	cga	tat	ggc	cta	gca	1728	
Ser	Thr	Gly	Ser	Val	Gly	Thr	Leu	Phe	Leu	Ala	Arg	Tyr	Gly	Leu	Ala		

565										570					575					
tta	gaa	aaa	gca	ggg	aaa	tat	cgt	gta	aga	ctg	aga	tat	gct	act	gat	1776				
Leu	Glu	Lys	Ala	Gly	Lys	Tyr	Arg	Val	Arg	Leu	Arg	Tyr	Ala	Thr	Asp					
			580					585					590							
gca	gat	att	gta	ttg	cat	gta	aac	gat	gct	cag	att	cag	atg	cca	aaa	1824				
Ala	Asp	Ile	Val	Leu	His	Val	Asn	Asp	Ala	Gln	Ile	Gln	Met	Pro	Lys					
		595					600					605								
aca	atg	aac	cca	ggg	gag	gat	ctg	aca	tct	aaa	act	ttt	aaa	gtt	gca	1872				
Thr	Met	Asn	Pro	Gly	Glu	Asp	Leu	Thr	Ser	Lys	Thr	Phe	Lys	Val	Ala					
	610					615					620									
gat	gct	atc	aca	aca	gtt	aat	tta	gca	aca	gat	agt	tcg	gtt	gca	gtt	1920				
Asp	Ala	Ile	Thr	Thr	Val	Asn	Leu	Ala	Thr	Asp	Ser	Ser	Val	Ala	Val					
625					630					635				640						
aaa	cat	aat	gta	ggg	gaa	gac	cct	aat	tca	aca	tta	tct	ggg	ata	gtt	1968				
Lys	His	Asn	Val	Gly	Glu	Asp	Pro	Asn	Ser	Thr	Leu	Ser	Gly	Ile	Val					
			645					650					655							
tac	gtt	gac	cga	atc	gaa	ttc	atc	cca	gta	gat	gag	aca	tat	gaa	gcg	2016				
Tyr	Val	Asp	Arg	Ile	Glu	Phe	Ile	Pro	Val	Asp	Glu	Thr	Tyr	Glu	Ala					
		660					665						670							
gaa																2019				
Glu																				

<210> 58
 <211> 673
 <212> PRT
 <213> Bacillus thuringiensis (mutated)

<400> 58

Met	Ser	Pro	Asn	Asn	Gln	Asn	Glu	Tyr	Glu	Ile	Ile	Asp	Ala	Thr	Pro
1				5					10					15	
Ser	Thr	Ser	Val	Ser	Asn	Asp	Ser	Asn	Arg	Tyr	Pro	Phe	Ala	Asn	Glu
			20					25					30		
Pro	Thr	Asn	Ala	Leu	Gln	Asn	Met	Asp	Tyr	Lys	Asp	Tyr	Ala	Val	Gly
		35				40					45				
Ser	Ala	Gly	Asn	Ala	Ser	Glu	Tyr	Pro	Gly	Ser	Pro	Glu	Val	Leu	Val
	50					55					60				
Ser	Gly	Gln	Asp	Ala	Ala	Lys	Ala	Ala	Ile	Asp	Ile	Val	Gly	Lys	Leu
65				70					75					80	
Leu	Ser	Gly	Leu	Gly	Val	Pro	Phe	Val	Gly	Pro	Ile	Val	Ser	Leu	Tyr
			85					90					95		
Thr	Gln	Leu	Ile	Asp	Ile	Leu	Trp	Pro	Ser	Gly	Glu	Lys	Ser	Gln	Trp
		100						105					110		
Glu	Ile	Phe	Met	Glu	Gln	Val	Glu	Glu	Leu	Ile	Asn	Gln	Lys	Ile	Ala
		115					120					125			
Glu	Tyr	Ala	Arg	Asn	Lys	Ala	Leu	Ser	Glu	Leu	Glu	Gly	Leu	Gly	Asn
	130					135					140				
Asn	Tyr	Gln	Leu	Tyr	Leu	Thr	Ala	Leu	Glu	Glu	Trp	Glu	Glu	Asn	Pro
145					150					155				160	

Phe	Arg	Arg	Gly	Phe	Arg	Arg	Gly	Ala	Leu	Arg	Asp	Val	Arg	Asn	Arg	165	170	175
Phe	Glu	Ile	Leu	Asp	Ser	Leu	Phe	Thr	Gln	Tyr	Met	Pro	Ser	Phe	Arg	180	185	190
Val	Thr	Asn	Phe	Glu	Val	Pro	Phe	Leu	Thr	Val	Tyr	Ala	Met	Ala	Ala	195	200	205
Asn	Leu	His	Leu	Leu	Leu	Leu	Lys	Asp	Ala	Ser	Ile	Phe	Gly	Glu	Glu	210	215	220
Trp	Gly	Trp	Ser	Thr	Thr	Thr	Ile	Asn	Asn	Tyr	Tyr	Asp	Arg	Gln	Met	225	230	235
Lys	Leu	Thr	Ala	Glu	Tyr	Ser	Asp	His	Cys	Val	Lys	Trp	Tyr	Glu	Thr	245	250	255
Gly	Leu	Ala	Lys	Leu	Lys	Gly	Thr	Ser	Ala	Lys	Gln	Trp	Val	Asp	Tyr	260	265	270
Asn	Gln	Phe	Arg	Arg	Glu	Met	Thr	Leu	Ala	Val	Leu	Asp	Val	Val	Ala	275	280	285
Leu	Phe	Pro	Asn	Tyr	Asp	Thr	Arg	Thr	Tyr	Pro	Met	Glu	Thr	Lys	Ala	290	295	300
Gln	Leu	Thr	Arg	Glu	Val	Tyr	Thr	Asp	Pro	Leu	Gly	Ala	Val	Asn	Val	305	310	315
Ser	Ser	Ile	Gly	Ser	Trp	Tyr	Asp	Lys	Ala	Pro	Ser	Phe	Gly	Val	Ile	325	330	335
Glu	Ser	Ser	Val	Ile	Arg	Pro	Pro	His	Val	Phe	Asp	Tyr	Ile	Thr	Gly	340	345	350
Leu	Thr	Val	Tyr	Thr	Gln	Ser	Arg	Ser	Ile	Ser	Ser	Ala	Arg	Tyr	Ile	355	360	365
Arg	His	Trp	Ala	Gly	His	Gln	Ile	Ser	Tyr	His	Arg	Val	Ser	Arg	Gly	370	375	380
Ser	Asn	Leu	Gln	Gln	Met	Tyr	Gly	Thr	Asn	Gln	Asn	Leu	His	Ser	Thr	385	390	395
Ser	Thr	Phe	Asp	Phe	Thr	Asn	Tyr	Asp	Ile	Tyr	Lys	Thr	Leu	Ser	Lys	405	410	415
Asp	Ala	Val	Leu	Leu	Asp	Ile	Val	Tyr	Pro	Gly	Tyr	Thr	Tyr	Ile	Phe	420	425	430
Phe	Gly	Met	Pro	Glu	Val	Glu	Phe	Phe	Met	Val	Asn	Gln	Leu	Asn	Asn	435	440	445
Thr	Arg	Lys	Thr	Leu	Lys	Tyr	Asn	Pro	Val	Ser	Lys	Asp	Ile	Ile	Ala	450	455	460
Ser	Thr	Arg	Asp	Ser	Glu	Leu	Glu	Leu	Pro	Pro	Glu	Thr	Ser	Asp	Gln	465	470	475
Pro	Asn	Tyr	Glu	Ser	Tyr	Ser	His	Arg	Leu	Cys	His	Ile	Thr	Ser	Ile	485	490	495
Pro	Ala	Thr	Gly	Asn	Thr	Thr	Gly	Leu	Val	Pro	Val	Phe	Ser	Trp	Thr	500	505	510
His	Arg	Ser	Ala	Asp	Leu	Asn	Asn	Thr	Ile	Tyr	Ser	Asp	Lys	Ile	Thr	515	520	525
Gln	Ile	Pro	Ala	Val	Lys	Cys	Trp	Asp	Asn	Leu	Pro	Phe	Val	Pro	Val	530	535	540
Val	Lys	Gly	Pro	Gly	His	Thr	Gly	Gly	Asp	Leu	Leu	Gln	Tyr	Asn	Arg	545	550	555
Ser	Thr	Gly	Ser	Val	Gly	Thr	Leu	Phe	Leu	Ala	Arg	Tyr	Gly	Leu	Ala	565	570	575
Leu	Glu	Lys	Ala	Gly	Lys	Tyr	Arg	Val	Arg	Leu	Arg	Tyr	Ala	Thr	Asp	580	585	590
Ala	Asp	Ile	Val	Leu	His	Val	Asn	Asp	Ala	Gln	Ile	Gln	Met	Pro	Lys	595	600	605
Thr	Met	Asn	Pro	Gly	Glu	Asp	Leu	Thr	Ser	Lys	Thr	Phe	Lys	Val	Ala			

610	615	620
Asp Ala Ile Thr Thr Val Asn Leu Ala Thr Asp Ser Ser Val Ala Val		
625	630	635
Lys His Asn Val Gly Glu Asp Pro Asn Ser Thr Leu Ser Gly Ile Val		640
	645	650
Tyr Val Asp Arg Ile Glu Phe Ile Pro Val Asp Glu Thr Tyr Glu Ala		655
	660	665
		670
Glu		

<210> 59
 <211> 2019
 <212> DNA
 <213> *Bacillus thuringiensis* (mutated)

<220>
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1 5 10 15	
tct act tct gta tcc aat gat tct aac aga tac cct ttt gcg aat gag	96
Ser Thr Ser Val Ser Asn Asp Ser Asn Arg Tyr Pro Phe Ala Asn Glu	
20 25 30	
cca aca aat gcg cta caa aat atg gat tat aaa gat tat tta aaa atg	144
Pro Thr Asn Ala Leu Gln Asn Met Asp Tyr Lys Asp Tyr Leu Lys Met	
35 40 45	
tct gcg gga aat gct agt gaa tac cct ggt tca cct gaa gta ctt gtt	192
Ser Ala Gly Asn Ala Ser Glu Tyr Pro Gly Ser Pro Glu Val Leu Val	
50 55 60	
agc gga caa gat gca gct aag gcc gca att gat ata gta ggt aaa tta	240
Ser Gly Gln Asp Ala Ala Lys Ala Ala Ile Asp Ile Val Gly Lys Leu	
65 70 75 80	
cta tca ggt tta ggg gtc cca ttt gtt ggg ccg ata gtg agt ctt tat	288
Leu Ser Gly Leu Gly Val Pro Phe Val Gly Pro Ile Val Ser Leu Tyr	
85 90 95	
act caa ctt att gat att ctg tgg cct tca ggg gaa aag agt caa tgg	336
Thr Gln Leu Ile Asp Ile Leu Trp Pro Ser Gly Glu Lys Ser Gln Trp	
100 105 110	
gaa att ttt atg gaa caa gta gaa gaa ctc att aat caa aaa ata gca	384
Glu Ile Phe Met Glu Gln Val Glu Glu Leu Ile Asn Gln Lys Ile Ala	
115 120 125	
gaa tat gca agg aat aaa gcg ctt tcg gaa tta gaa gga tta ggt aat	432
Glu Tyr Ala Arg Asn Lys Ala Leu Ser Glu Leu Glu Gly Leu Gly Asn	
130 135 140	

aat tac caa tta tat cta act gcg ctt gaa gaa tgg gaa gaa aat cca	480
Asn Tyr Gln Leu Tyr Leu Thr Ala Leu Glu Trp Glu Glu Asn Pro	
145 150 155 160	
ttt cga cga ggt ttt cga cga ggt gcc tta cga gat gtg cga aat cga	528
Phe Arg Arg Gly Phe Arg Arg Gly Ala Leu Arg Asp Val Arg Asn Arg	
165 170 175	
ttt gaa atc ctg gat agt tta ttt acg caa tat atg cca tct ttt aga	576
Phe Glu Ile Leu Asp Ser Leu Phe Thr Gln Tyr Met Pro Ser Phe Arg	
180 185 190	
gtg aca aat ttt gaa gta cca ttc ctt act gta tat gca atg gca gcc	624
Val Thr Asn Phe Glu Val Pro Phe Leu Thr Val Tyr Ala Met Ala Ala	
195 200 205	
aac ctt cat tta ctg tta tta aag gac gcg tca att ttt gga gaa gaa	672
Asn Leu His Leu Leu Leu Lys Asp Ala Ser Ile Phe Gly Glu Glu	
210 215 220	
tgg gga tgg tca aca act act att aat aac tat tat gat cgt caa atg	720
Trp Gly Trp Ser Thr Thr Thr Ile Asn Asn Tyr Tyr Asp Arg Gln Met	
225 230 235 240	
aaa ctt act gca gaa tat tct gat cac tgt gta aag tgg tat gaa act	768
Lys Leu Thr Ala Glu Tyr Ser Asp His Cys Val Lys Trp Tyr Glu Thr	
245 250 255	
ggt tta gca aaa tta aaa ggc acg agc gct aaa caa tgg gtt gac tat	816
Gly Leu Ala Lys Leu Lys Gly Thr Ser Ala Lys Gln Trp Val Asp Tyr	
260 265 270	
aac caa ttc cgt aga gaa atg aca ctg gcg gtt tta gat gtt gtt gca	864
Asn Gln Phe Arg Arg Glu Met Thr Leu Ala Val Leu Asp Val Val Ala	
275 280 285	
tta ttc cca aat tat gac aca ata acg tac cca atg gaa acg aaa gca	912
Leu Phe Pro Asn Tyr Asp Thr Ile Thr Tyr Pro Met Glu Thr Lys Ala	
290 295 300	
caa cta aca agg gaa gta tat aca gat cca ctg ggc gcg gta aac gtg	960
Gln Leu Thr Arg Glu Val Tyr Thr Asp Pro Leu Gly Ala Val Asn Val	
305 310 315 320	
tct tca att ggt tcc tgg tat gac aaa gca cct tct ttc gga gtg ata	1008
Ser Ser Ile Gly Ser Trp Tyr Asp Lys Ala Pro Ser Phe Gly Val Ile	
325 330 335	
gaa tca tcc gtt att cga cca ccc cat gta ttt gat tat ata acg gga	1056
Glu Ser Ser Val Ile Arg Pro Pro His Val Phe Asp Tyr Ile Thr Gly	
340 345 350	
ctc aca gtg tat aca caa tca aga agc att tct tcc gct cgc tat ata	1104
Leu Thr Val Tyr Thr Gln Ser Arg Ser Ile Ser Ser Ala Arg Tyr Ile	
355 360 365	
aga cat tgg gct ggt cat caa ata agc tac cat cgt gtc agt agg ggt	1152

Arg	His	Trp	Ala	Gly	His	Gln	Ile	Ser	Tyr	His	Arg	Val	Ser	Arg	Gly		
370						375					380						
agt	aat	ctt	caa	caa	atg	tat	gga	act	aat	caa	aat	cta	cac	agc	act	1200	
Ser	Asn	Leu	Gln	Gln	Met	Tyr	Gly	Thr	Asn	Gln	Asn	Leu	His	Ser	Thr		
385					390					395					400		
agt	acc	ttt	gat	ttt	acg	aat	tat	gat	att	tac	aag	act	cta	tca	aag	1248	
Ser	Thr	Phe	Asp	Phe	Thr	Asn	Tyr	Asp	Ile	Tyr	Lys	Thr	Leu	Ser	Lys		
				405					410					415			
gat	gca	gta	ctc	ctt	gat	att	gtt	tac	cct	ggt	tat	acg	tat	ata	ttt	1296	
Asp	Ala	Val	Leu	Leu	Asp	Ile	Val	Tyr	Pro	Gly	Tyr	Thr	Tyr	Ile	Phe		
			420					425					430				
ttt	gga	atg	cca	gaa	gtc	gag	ttt	ttc	atg	gta	aac	caa	ttg	aat	aat	1344	
Phe	Gly	Met	Pro	Glu	Val	Glu	Phe	Phe	Met	Val	Asn	Gln	Leu	Asn	Asn		
	435					440						445					
acc	aga	aag	acg	tta	aag	tat	aat	cca	gtt	tcc	aaa	gat	att	ata	gcg	1392	
Thr	Arg	Lys	Thr	Leu	Lys	Tyr	Asn	Pro	Val	Ser	Lys	Asp	Ile	Ile	Ala		
	450					455					460						
agt	aca	aga	gat	tcg	gaa	tta	gaa	tta	cct	cca	gaa	act	tca	gat	caa	1440	
Ser	Thr	Arg	Asp	Ser	Glu	Leu	Glu	Leu	Pro	Pro	Glu	Thr	Ser	Asp	Gln		
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cca	aat	tat	gag	tca	tat	agc	cat	aga	tta	tgt	cat	atc	aca	agt	att	1488	
Pro	Asn	Tyr	Glu	Ser	Tyr	Ser	His	Arg	Leu	Cys	His	Ile	Thr	Ser	Ile		
				485					490					495			
ccc	gcg	acg	ggt	aac	act	acc	gga	tta	gta	cct	gta	ttt	tct	tgg	aca	1536	
Pro	Ala	Thr	Gly	Asn	Thr	Thr	Gly	Leu	Val	Pro	Val	Phe	Ser	Trp	Thr		
			500					505					510				
cat	cga	agt	gca	gat	tta	aac	aat	aca	ata	tat	tca	gat	aaa	atc	act	1584	
His	Arg	Ser	Ala	Asp	Leu	Asn	Asn	Thr	Ile	Tyr	Ser	Asp	Lys	Ile	Thr		
			515				520					525					
caa	att	ccg	gcc	gtt	aaa	tgt	tgg	gat	aat	tta	ccg	ttt	gtt	cca	gtg	1632	
Gln	Ile	Pro	Ala	Val	Lys	Cys	Trp	Asp	Asn	Leu	Pro	Phe	Val	Pro	Val		
	530					535					540						
gta	aaa	gga	cca	gga	cat	aca	gga	ggg	gat	tta	tta	cag	tat	aat	aga	1680	
Val	Lys	Gly	Pro	Gly	His	Thr	Gly	Gly	Asp	Leu	Leu	Gln	Tyr	Asn	Arg		
545					550					555					560		
agt	act	ggt	tct	gta	gga	acc	tta	ttt	cta	gct	cga	tat	ggc	cta	gca	1728	
Ser	Thr	Gly	Ser	Val	Gly	Thr	Leu	Phe	Leu	Ala	Arg	Tyr	Gly	Leu	Ala		
				565					570					575			
tta	gaa	aaa	gca	ggg	aaa	tat	cgt	gta	aga	ctg	aga	tat	gct	act	gat	1776	
Leu	Glu	Lys	Ala	Gly	Lys	Tyr	Arg	Val	Arg	Leu	Arg	Tyr	Ala	Thr	Asp		
			580					585					590				
gca	gat	att	gta	ttg	cat	gta	aac	gat	gct	cag	att	cag	atg	cca	aaa	1824	
Ala	Asp	Ile	Val	Leu	His	Val	Asn	Asp	Ala	Gln	Ile	Gln	Met	Pro	Lys		

595	600	605	
aca atg aac cca ggt gag gat ctg aca tct aaa act ttt aaa gtt gca			1872
Thr Met Asn Pro Gly Glu Asp Leu Thr Ser Lys Thr Phe Lys Val Ala			
610	615	620	
gat gct atc aca aca gtt aat tta gca aca gat agt tcg gtt gca gtt			1920
Asp Ala Ile Thr Thr Val Asn Leu Ala Thr Asp Ser Ser Val Ala Val			
625	630	635	640
aaa cat aat gta ggt gaa gac cct aat tca aca tta tct ggt ata gtt			1968
Lys His Asn Val Gly Glu Asp Pro Asn Ser Thr Leu Ser Gly Ile Val			
	645	650	655
tac gtt gac cga atc gaa ttc atc cca gta gat gag aca tat gaa gcg			2016
Tyr Val Asp Arg Ile Glu Phe Ile Pro Val Asp Glu Thr Tyr Glu Ala			
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gaa			2019
Glu			

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 <212> PRT
 <213> *Bacillus thuringiensis* (mutated)

<400> 60

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Pro Thr Asn Ala Leu Gln Asn Met Asp Tyr Lys Asp Tyr Leu Lys Met			
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Ser Ala Gly Asn Ala Ser Glu Tyr Pro Gly Ser Pro Glu Val Leu Val			
	50	55	60
Ser Gly Gln Asp Ala Ala Lys Ala Ala Ile Asp Ile Val Gly Lys Leu			
65	70	75	80
Leu Ser Gly Leu Gly Val Pro Phe Val Gly Pro Ile Val Ser Leu Tyr			
	85	90	95
Thr Gln Leu Ile Asp Ile Leu Trp Pro Ser Gly Glu Lys Ser Gln Trp			
	100	105	110
Glu Ile Phe Met Glu Gln Val Glu Leu Ile Asn Gln Lys Ile Ala			
	115	120	125
Glu Tyr Ala Arg Asn Lys Ala Leu Ser Glu Leu Glu Gly Leu Gly Asn			
	130	135	140
Asn Tyr Gln Leu Tyr Leu Thr Ala Leu Glu Glu Trp Glu Glu Asn Pro			
145	150	155	160
Phe Arg Arg Gly Phe Arg Arg Gly Ala Leu Arg Asp Val Arg Asn Arg			
	165	170	175
Phe Glu Ile Leu Asp Ser Leu Phe Thr Gln Tyr Met Pro Ser Phe Arg			
	180	185	190
Val Thr Asn Phe Glu Val Pro Phe Leu Thr Val Tyr Ala Met Ala Ala			
	195	200	205
Asn Leu His Leu Leu Leu Leu Lys Asp Ala Ser Ile Phe Gly Glu Glu			
210	215	220	

Trp	Gly	Trp	Ser	Thr	Thr	Thr	Ile	Asn	Asn	Tyr	Tyr	Asp	Arg	Gln	Met
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				245					250						255
Gly	Leu	Ala	Lys	Leu	Lys	Gly	Thr	Ser	Ala	Lys	Gln	Trp	Val	Asp	Tyr
			260					265					270		
Asn	Gln	Phe	Arg	Arg	Glu	Met	Thr	Leu	Ala	Val	Leu	Asp	Val	Val	Ala
		275					280					285			
Leu	Phe	Pro	Asn	Tyr	Asp	Thr	Ile	Thr	Tyr	Pro	Met	Glu	Thr	Lys	Ala
	290					295				300					
Gln	Leu	Thr	Arg	Glu	Val	Tyr	Thr	Asp	Pro	Leu	Gly	Ala	Val	Asn	Val
305					310					315					320
Ser	Ser	Ile	Gly	Ser	Trp	Tyr	Asp	Lys	Ala	Pro	Ser	Phe	Gly	Val	Ile
				325					330					335	
Glu	Ser	Ser	Val	Ile	Arg	Pro	Pro	His	Val	Phe	Asp	Tyr	Ile	Thr	Gly
			340					345					350		
Leu	Thr	Val	Tyr	Thr	Gln	Ser	Arg	Ser	Ile	Ser	Ser	Ala	Arg	Tyr	Ile
		355					360					365			
Arg	His	Trp	Ala	Gly	His	Gln	Ile	Ser	Tyr	His	Arg	Val	Ser	Arg	Gly
	370					375					380				
Ser	Asn	Leu	Gln	Gln	Met	Tyr	Gly	Thr	Asn	Gln	Asn	Leu	His	Ser	Thr
385					390					395					400
Ser	Thr	Phe	Asp	Phe	Thr	Asn	Tyr	Asp	Ile	Tyr	Lys	Thr	Leu	Ser	Lys
				405					410					415	
Asp	Ala	Val	Leu	Leu	Asp	Ile	Val	Tyr	Pro	Gly	Tyr	Thr	Tyr	Ile	Phe
			420					425					430		
Phe	Gly	Met	Pro	Glu	Val	Glu	Phe	Phe	Met	Val	Asn	Gln	Leu	Asn	Asn
		435					440					445			
Thr	Arg	Lys	Thr	Leu	Lys	Tyr	Asn	Pro	Val	Ser	Lys	Asp	Ile	Ile	Ala
	450					455					460				
Ser	Thr	Arg	Asp	Ser	Glu	Leu	Glu	Leu	Pro	Pro	Glu	Thr	Ser	Asp	Gln
465					470					475					480
Pro	Asn	Tyr	Glu	Ser	Tyr	Ser	His	Arg	Leu	Cys	His	Ile	Thr	Ser	Ile
				485					490					495	
Pro	Ala	Thr	Gly	Asn	Thr	Thr	Gly	Leu	Val	Pro	Val	Phe	Ser	Trp	Thr
			500					505					510		
His	Arg	Ser	Ala	Asp	Leu	Asn	Asn	Thr	Ile	Tyr	Ser	Asp	Lys	Ile	Thr
		515					520					525			
Gln	Ile	Pro	Ala	Val	Lys	Cys	Trp	Asp	Asn	Leu	Pro	Phe	Val	Pro	Val
	530					535					540				
Val	Lys	Gly	Pro	Gly	His	Thr	Gly	Gly	Asp	Leu	Leu	Gln	Tyr	Asn	Arg
545					550					555					560
Ser	Thr	Gly	Ser	Val	Gly	Thr	Leu	Phe	Leu	Ala	Arg	Tyr	Gly	Leu	Ala
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			580					585					590		
Ala	Asp	Ile	Val	Leu	His	Val	Asn	Asp	Ala	Gln	Ile	Gln	Met	Pro	Lys
		595					600					605			
Thr	Met	Asn	Pro	Gly	Glu	Asp	Leu	Thr	Ser	Lys	Thr	Phe	Lys	Val	Ala
	610					615					620				
Asp	Ala	Ile	Thr	Thr	Val	Asn	Leu	Ala	Thr	Asp	Ser	Ser	Val	Ala	Val
625					630					635					640
Lys	His	Asn	Val	Gly	Glu	Asp	Pro	Asn	Ser	Thr	Leu	Ser	Gly	Ile	Val
				645					650					655	
Tyr	Val	Asp	Arg	Ile	Glu	Phe	Ile	Pro	Val	Asp	Glu	Thr	Tyr	Glu	Ala
			660					665					670		
Glu															

<210> 61
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 <213> *Bacillus thuringiensis* (mutated)

<220>
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tct act tct gta tcc aat gat tct aac aga tac cct ttt gcg aat gag 96
Ser Thr Ser Val Ser Asn Asp Ser Asn Arg Tyr Pro Phe Ala Asn Glu
20 25 30

cca aca aat gcg cta caa aat atg gat tat aaa gat tat tta aaa atg 144
Pro Thr Asn Ala Leu Gln Asn Met Asp Tyr Lys Asp Tyr Leu Lys Met
35 40 45

tct gcg gga aat gct agt gaa tac cct ggt tca cct gaa gta ctt gtt 192
Ser Ala Gly Asn Ala Ser Glu Tyr Pro Gly Ser Pro Glu Val Leu Val
50 55 60

agc gga caa gat gca gct aag gcc gca att gat ata gta ggt aaa tta 240
Ser Gly Gln Asp Ala Ala Lys Ala Ala Ile Asp Ile Val Gly Lys Leu
65 70 75 80

cta tca ggt tta ggg gtc cca ttt gtt ggg ccg ata gtg agt ctt tat 288
Leu Ser Gly Leu Gly Val Pro Phe Val Gly Pro Ile Val Ser Leu Tyr
85 90 95

act caa ctt att gat att ctg tgg cct tca ggg gaa aag agt caa tgg 336
Thr Gln Leu Ile Asp Ile Leu Trp Pro Ser Gly Glu Lys Ser Gln Trp
100 105 110

gaa att ttt atg gaa caa gta gaa gaa ctc att aat caa aaa ata gca 384
Glu Ile Phe Met Glu Gln Val Glu Glu Leu Ile Asn Gln Lys Ile Ala
115 120 125

gaa tat gca agg aat aaa gcg ctt tcg gaa tta gaa gga tta ggt aat 432
Glu Tyr Ala Arg Asn Lys Ala Leu Ser Glu Leu Glu Gly Leu Gly Asn
130 135 140

aat tac caa tta tat cta act gcg ctt gaa gaa tgg gaa gaa aat cca 480
Asn Tyr Gln Leu Tyr Leu Thr Ala Leu Glu Glu Trp Glu Glu Asn Pro
145 150 155 160

ttt cga cga ggt ttt cga cga ggt gcc tta cga gat gtg cga aat cga 528
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165 170 175

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Phe Glu Ile Leu Asp Ser Leu Phe Thr Gln Tyr Met Pro Ser Phe Arg	
180 185 190	
gtg aca aat ttt gaa gta cca ttc ctt act gta tat gca atg gca gcc	624
Val Thr Asn Phe Glu Val Pro Phe Leu Thr Val Tyr Ala Met Ala Ala	
195 200 205	
aac ctt cat tta ctg tta tta aag gac gcg tca att ttt gga gaa gaa	672
Asn Leu His Leu Leu Leu Leu Lys Asp Ala Ser Ile Phe Gly Glu Glu	
210 215 220	
tgg gga tgg tca aca act act att aat aac gtg gtg gat cgt caa atg	720
Trp Gly Trp Ser Thr Thr Thr Ile Asn Asn Val Val Asp Arg Gln Met	
225 230 235 240	
aaa ctt act gca gaa tat tct gat cac tgt gta aag tgg tat gaa act	768
Lys Leu Thr Ala Glu Tyr Ser Asp His Cys Val Lys Trp Tyr Glu Thr	
245 250 255	
ggg tta gca aaa tta aaa ggc acg agc gct aaa caa tgg gtt gac tat	816
Gly Leu Ala Lys Leu Lys Gly Thr Ser Ala Lys Gln Trp Val Asp Tyr	
260 265 270	
aac caa ttc cgt aga gaa atg aca ctg gcg gtt tta gat gtt gtt gca	864
Asn Gln Phe Arg Arg Glu Met Thr Leu Ala Val Leu Asp Val Val Ala	
275 280 285	
tta ttc cca aat tat gac aca ata acg tac cca ata gaa acg aaa gca	912
Leu Phe Pro Asn Tyr Asp Thr Thr Thr Tyr Pro Ile Glu Thr Lys Ala	
290 295 300	
caa cta aca agg gaa gta tat aca gat cca ctg ggc gcg gta aac gtg	960
Gln Leu Thr Arg Glu Val Tyr Thr Asp Pro Leu Gly Ala Val Asn Val	
305 310 315 320	
tct tca att ggt tcc tgg tat gac aaa gca cct tct ttc gga gtg ata	1008
Ser Ser Ile Gly Ser Trp Tyr Asp Lys Ala Pro Ser Phe Gly Val Ile	
325 330 335	
gaa tca tcc gtt att cga cca ccc cat gta ttt gat tat ata acg gga	1056
Glu Ser Ser Val Ile Arg Pro Pro His Val Phe Asp Tyr Ile Thr Gly	
340 345 350	
ctc aca gtg tat aca caa tca aga agc att tct tcc gct cgc tat ata	1104
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355 360 365	
aga cat tgg gct ggt cat caa ata agc tac cat cgt gtc agt agg ggt	1152
Arg His Trp Ala Gly His Gln Ile Ser Tyr His Arg Val Ser Arg Gly	
370 375 380	
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Ser Asn Leu Gln Gln Met Tyr Gly Thr Asn Gln Asn Leu His Ser Thr	
385 390 395 400	
agt acc ttt gat ttt acg aat tat gat att tac aag act cta tca aag	1248

Ser	Thr	Phe	Asp	Phe	Thr	Asn	Tyr	Asp	Ile	Tyr	Lys	Thr	Leu	Ser	Lys	
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gat	gca	gta	ctc	ctt	gat	att	gtt	tac	cct	ggg	tat	acg	tat	ata	ttt	1296
Asp	Ala	Val	Leu	Leu	Asp	Ile	Val	Tyr	Pro	Gly	Tyr	Thr	Tyr	Ile	Phe	
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ttt	gga	atg	cca	gaa	gtc	gag	ttt	ttc	atg	gta	aac	caa	ttg	aat	aat	1344
Phe	Gly	Met	Pro	Glu	Val	Glu	Phe	Phe	Met	Val	Asn	Gln	Leu	Asn	Asn	
		435					440					445				
acc	aga	aag	acg	tta	aag	tat	aat	cca	gtt	tcc	aaa	gat	att	ata	gcg	1392
Thr	Arg	Lys	Thr	Leu	Lys	Tyr	Asn	Pro	Val	Ser	Lys	Asp	Ile	Ile	Ala	
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agt	aca	aga	gat	tcg	gaa	tta	gaa	tta	cct	cca	gaa	act	tca	gat	caa	1440
Ser	Thr	Arg	Asp	Ser	Glu	Leu	Glu	Leu	Pro	Pro	Glu	Thr	Ser	Asp	Gln	
465					470					475					480	
cca	aat	tat	gag	tca	tat	agc	cat	aga	tta	tgt	cat	atc	aca	agt	att	1488
Pro	Asn	Tyr	Glu	Ser	Tyr	Ser	His	Arg	Leu	Cys	His	Ile	Thr	Ser	Ile	
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ccc	gcg	acg	ggg	aac	act	acc	gga	tta	gta	cct	gta	ttt	tct	tggt	aca	1536
Pro	Ala	Thr	Gly	Asn	Thr	Thr	Gly	Leu	Val	Pro	Val	Phe	Ser	Trp	Thr	
			500					505					510			
cat	cga	agt	gca	gat	tta	aac	aat	aca	ata	tat	tca	gat	aaa	atc	act	1584
His	Arg	Ser	Ala	Asp	Leu	Asn	Asn	Thr	Ile	Tyr	Ser	Asp	Lys	Ile	Thr	
		515					520					525				
caa	att	ccg	gcc	gtt	aaa	tgt	tggt	gat	aat	tta	ccg	ttt	gtt	cca	gtg	1632
Gln	Ile	Pro	Ala	Val	Lys	Cys	Trp	Asp	Asn	Leu	Pro	Phe	Val	Pro	Val	
	530					535					540					
gta	aaa	gga	cca	gga	cat	aca	gga	ggg	gat	tta	tta	cag	tat	aat	aga	1680
Val	Lys	Gly	Pro	Gly	His	Thr	Gly	Gly	Asp	Leu	Leu	Gln	Tyr	Asn	Arg	
545					550				555						560	
agt	act	ggg	tct	gta	gga	acc	tta	ttt	cta	gct	cga	tat	ggc	cta	gca	1728
Ser	Thr	Gly	Ser	Val	Gly	Thr	Leu	Phe	Leu	Ala	Arg	Tyr	Gly	Leu	Ala	
				565					570					575		
tta	gaa	aaa	gca	ggg	aaa	tat	cgt	gta	aga	ctg	aga	tat	gct	act	gat	1776
Leu	Glu	Lys	Ala	Gly	Lys	Tyr	Arg	Val	Arg	Leu	Arg	Tyr	Ala	Thr	Asp	
			580					585					590			
gca	gat	att	gta	ttg	cat	gta	aac	gat	gct	cag	att	cag	atg	cca	aaa	1824
Ala	Asp	Ile	Val	Leu	His	Val	Asn	Asp	Ala	Gln	Ile	Gln	Met	Pro	Lys	
		595					600					605				
aca	atg	aac	cca	ggg	gag	gat	ctg	aca	tct	aaa	act	ttt	aaa	gtt	gca	1872
Thr	Met	Asn	Pro	Gly	Glu	Asp	Leu	Thr	Ser	Lys	Thr	Phe	Lys	Val	Ala	
	610					615					620					
gat	gct	atc	aca	aca	gtt	aat	tta	gca	aca	gat	agt	tcg	gtt	gca	gtt	1920
Asp	Ala	Ile	Thr	Thr	Val	Asn	Leu	Ala	Thr	Asp	Ser	Ser	Val	Ala	Val	

625	630	635	640	
aaa cat aat gta ggt gaa gac cct aat tca aca tta tct ggt ata gtt				1968
Lys His Asn Val Gly Glu Asp Pro Asn Ser Thr Leu Ser Gly Ile Val				
	645	650	655	
tac gtt gac cga atc gaa ttc atc cca gta gat gag aca tat gaa gcg				2016
Tyr Val Asp Arg Ile Glu Phe Ile Pro Val Asp Glu Thr Tyr Glu Ala				
	660	665	670	
gaa				2019
Glu				

<210> 62
 <211> 673
 <212> PRT
 <213> Bacillus thuringiensis (mutated)

<400> 62

Met	Ser	Pro	Asn	Asn	Gln	Asn	Glu	Tyr	Glu	Ile	Ile	Asp	Ala	Thr	Pro
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Ser	Thr	Ser	Val	Ser	Asn	Asp	Ser	Asn	Arg	Tyr	Pro	Phe	Ala	Asn	Glu
			20					25					30		
Pro	Thr	Asn	Ala	Leu	Gln	Asn	Met	Asp	Tyr	Lys	Asp	Tyr	Leu	Lys	Met
		35					40					45			
Ser	Ala	Gly	Asn	Ala	Ser	Glu	Tyr	Pro	Gly	Ser	Pro	Glu	Val	Leu	Val
	50					55					60				
Ser	Gly	Gln	Asp	Ala	Ala	Lys	Ala	Ala	Ile	Asp	Ile	Val	Gly	Lys	Leu
65				70					75						80
Leu	Ser	Gly	Leu	Gly	Val	Pro	Phe	Val	Gly	Pro	Ile	Val	Ser	Leu	Tyr
			85						90					95	
Thr	Gln	Leu	Ile	Asp	Ile	Leu	Trp	Pro	Ser	Gly	Glu	Lys	Ser	Gln	Trp
		100						105					110		
Glu	Ile	Phe	Met	Glu	Gln	Val	Glu	Glu	Leu	Ile	Asn	Gln	Lys	Ile	Ala
	115						120					125			
Glu	Tyr	Ala	Arg	Asn	Lys	Ala	Leu	Ser	Glu	Leu	Glu	Gly	Leu	Gly	Asn
	130					135					140				
Asn	Tyr	Gln	Leu	Tyr	Leu	Thr	Ala	Leu	Glu	Glu	Trp	Glu	Glu	Asn	Pro
145					150					155					160
Phe	Arg	Arg	Gly	Phe	Arg	Arg	Gly	Ala	Leu	Arg	Asp	Val	Arg	Asn	Arg
			165						170					175	
Phe	Glu	Ile	Leu	Asp	Ser	Leu	Phe	Thr	Gln	Tyr	Met	Pro	Ser	Phe	Arg
		180						185					190		
Val	Thr	Asn	Phe	Glu	Val	Pro	Phe	Leu	Thr	Val	Tyr	Ala	Met	Ala	Ala
		195					200					205			
Asn	Leu	His	Leu	Leu	Leu	Leu	Lys	Asp	Ala	Ser	Ile	Phe	Gly	Glu	Glu
	210					215					220				
Trp	Gly	Trp	Ser	Thr	Thr	Thr	Ile	Asn	Asn	Val	Val	Asp	Arg	Gln	Met
225					230					235					240
Lys	Leu	Thr	Ala	Glu	Tyr	Ser	Asp	His	Cys	Val	Lys	Trp	Tyr	Glu	Thr
			245						250					255	
Gly	Leu	Ala	Lys	Leu	Lys	Gly	Thr	Ser	Ala	Lys	Gln	Trp	Val	Asp	Tyr
		260						265					270		
Asn	Gln	Phe	Arg	Arg	Glu	Met	Thr	Leu	Ala	Val	Leu	Asp	Val	Val	Ala
		275					280					285			

Leu Phe Pro Asn Tyr Asp Thr Ile Thr Tyr Pro Ile Glu Thr Lys Ala
 290 295 300
 Gln Leu Thr Arg Glu Val Tyr Thr Asp Pro Leu Gly Ala Val Asn Val
 305 310 315 320
 Ser Ser Ile Gly Ser Trp Tyr Asp Lys Ala Pro Ser Phe Gly Val Ile
 325 330 335
 Glu Ser Ser Val Ile Arg Pro Pro His Val Phe Asp Tyr Ile Thr Gly
 340 345 350
 Leu Thr Val Tyr Thr Gln Ser Arg Ser Ile Ser Ser Ala Arg Tyr Ile
 355 360 365
 Arg His Trp Ala Gly His Gln Ile Ser Tyr His Arg Val Ser Arg Gly
 370 375 380
 Ser Asn Leu Gln Gln Met Tyr Gly Thr Asn Gln Asn Leu His Ser Thr
 385 390 395 400
 Ser Thr Phe Asp Phe Thr Asn Tyr Asp Ile Tyr Lys Thr Leu Ser Lys
 405 410 415
 Asp Ala Val Leu Leu Asp Ile Val Tyr Pro Gly Tyr Thr Tyr Ile Phe
 420 425 430
 Phe Gly Met Pro Glu Val Glu Phe Phe Met Val Asn Gln Leu Asn Asn
 435 440 445
 Thr Arg Lys Thr Leu Lys Tyr Asn Pro Val Ser Lys Asp Ile Ile Ala
 450 455 460
 Ser Thr Arg Asp Ser Glu Leu Glu Leu Pro Pro Glu Thr Ser Asp Gln
 465 470 475 480
 Pro Asn Tyr Glu Ser Tyr Ser His Arg Leu Cys His Ile Thr Ser Ile
 485 490 495
 Pro Ala Thr Gly Asn Thr Thr Gly Leu Val Pro Val Phe Ser Trp Thr
 500 505 510
 His Arg Ser Ala Asp Leu Asn Asn Thr Ile Tyr Ser Asp Lys Ile Thr
 515 520 525
 Gln Ile Pro Ala Val Lys Cys Trp Asp Asn Leu Pro Phe Val Pro Val
 530 535 540
 Val Lys Gly Pro Gly His Thr Gly Gly Asp Leu Leu Gln Tyr Asn Arg
 545 550 555 560
 Ser Thr Gly Ser Val Gly Thr Leu Phe Leu Ala Arg Tyr Gly Leu Ala
 565 570 575
 Leu Glu Lys Ala Gly Lys Tyr Arg Val Arg Leu Arg Tyr Ala Thr Asp
 580 585 590
 Ala Asp Ile Val Leu His Val Asn Asp Ala Gln Ile Gln Met Pro Lys
 595 600 605
 Thr Met Asn Pro Gly Glu Asp Leu Thr Ser Lys Thr Phe Lys Val Ala
 610 615 620
 Asp Ala Ile Thr Thr Val Asn Leu Ala Thr Asp Ser Ser Val Ala Val
 625 630 635 640
 Lys His Asn Val Gly Glu Asp Pro Asn Ser Thr Leu Ser Gly Ile Val
 645 650 655
 Tyr Val Asp Arg Ile Glu Phe Ile Pro Val Asp Glu Thr Tyr Glu Ala
 660 665 670
 Glu

<210> 63
 <211> 2022
 <212> DNA
 <213> *Bacillus thuringiensis* (mutated)

<220>

<221> CDS

<222> (1)...(2022)

<400> 63

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Met Ser Pro Asn Asn Gln Asn Glu Tyr Glu Ile Ile Asp Ala Thr Pro	
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agc acc agc gtg agc aac gac agc aac agg tac cca ttc gcc aac gag	96
Ser Thr Ser Val Ser Asn Asp Ser Asn Arg Tyr Pro Phe Ala Asn Glu	
20 25 30	
cca acc aac gcc ctg cag aac atg gac tac aag gac tac ctg aag atg	144
Pro Thr Asn Ala Leu Gln Asn Met Asp Tyr Lys Asp Tyr Leu Lys Met	
35 40 45	
agc gcc ggc aac gcc agc gag tac cca ggc agc cca gag gtg ctg gtg	192
Ser Ala Gly Asn Ala Ser Glu Tyr Pro Gly Ser Pro Glu Val Leu Val	
50 55 60	
agc ggc cag gac gcc gcc aag gcc gcc atc gac atc gtg ggc aag ctg	240
Ser Gly Gln Asp Ala Ala Lys Ala Ala Ile Asp Ile Val Gly Lys Leu	
65 70 75 80	
ctg agc ggc ctg ggc gtg cca ttc gtg ggc cca atc gtg agc ctg tac	288
Leu Ser Gly Leu Gly Val Pro Phe Val Gly Pro Ile Val Ser Leu Tyr	
85 90 95	
acc cag ctg atc gac atc ctg tgg cca agc ggc gag aag agc cag tgg	336
Thr Gln Leu Ile Asp Ile Leu Trp Pro Ser Gly Glu Lys Ser Gln Trp	
100 105 110	
gag atc ttc atg gag cag gtg gag gag ctg atc aac cag aag atc gcc	384
Glu Ile Phe Met Glu Gln Val Glu Glu Leu Ile Asn Gln Lys Ile Ala	
115 120 125	
gag tac gcc agg aac aag gcc ctg agc gag ctg gag ggc ctg ggc aac	432
Glu Tyr Ala Arg Asn Lys Ala Leu Ser Glu Leu Glu Gly Leu Gly Asn	
130 135 140	
aac tac cag ctg tac ctg acc gcc ctg gag gag tgg gag gag aac cca	480
Asn Tyr Gln Leu Tyr Leu Thr Ala Leu Glu Glu Trp Glu Glu Asn Pro	
145 150 155 160	
ttc agg agg ggc ttc agg agg ggc gcc ctg agg gac gtg agg aac agg	528
Phe Arg Arg Gly Phe Arg Arg Gly Ala Leu Arg Asp Val Arg Asn Arg	
165 170 175	
ttc gag atc ctg gac agc ctg ttc acc cag tac atg cca agc ttc agg	576
Phe Glu Ile Leu Asp Ser Leu Phe Thr Gln Tyr Met Pro Ser Phe Arg	
180 185 190	
gtg acc aac ttc gag gtg cca ttc ctg acc gtg tac gcc atg gcc gcc	624
Val Thr Asn Phe Glu Val Pro Phe Leu Thr Val Tyr Ala Met Ala Ala	
195 200 205	

aac ctg cac ctg ctg ctg ctg aag gac gcc agc atc ttc ggc gag gag	672
Asn Leu His Leu Leu Leu Lys Asp Ala Ser Ile Phe Gly Glu Glu	
210 215 220	
tgg ggc tgg agc acc acc acc atc aac aac tac tac gac agg cag atg	720
Trp Gly Trp Ser Thr Thr Thr Ile Asn Asn Tyr Tyr Asp Arg Gln Met	
225 230 235 240	
aag ctg acc gcc gag tac agc gac cac tgc gtg aag tgg tac gag acc	768
Lys Leu Thr Ala Glu Tyr Ser Asp His Cys Val Lys Trp Tyr Glu Thr	
245 250 255	
ggc ctg gcc aag ctg aag ggc acc agc gcc aag cag tgg gtg gac tac	816
Gly Leu Ala Lys Leu Lys Gly Thr Ser Ala Lys Gln Trp Val Asp Tyr	
260 265 270	
aac cag ttc agg agg gag atg acc ctg gcc gtg ctg gac gtg gtg gcc	864
Asn Gln Phe Arg Arg Glu Met Thr Leu Ala Val Leu Asp Val Val Ala	
275 280 285	
ctg ttc cca aac tac gac acc agg acc tac cca atg gag acc aag gcc	912
Leu Phe Pro Asn Tyr Asp Thr Arg Thr Tyr Pro Met Glu Thr Lys Ala	
290 295 300	
cag ctg acc agg gag gtg tac acc gac cca ctg ggc gcc gtg aac gtg	960
Gln Leu Thr Arg Glu Val Tyr Thr Asp Pro Leu Gly Ala Val Asn Val	
305 310 315 320	
agc agc atc ggc agc tgg tac gac aag gcc cca agc ttc ggc gtg atc	1008
Ser Ser Ile Gly Ser Trp Tyr Asp Lys Ala Pro Ser Phe Gly Val Ile	
325 330 335	
gag agc agc gtg atc agg cca cca cac gtg ttc gac tac atc acc ggc	1056
Glu Ser Ser Val Ile Arg Pro Pro His Val Phe Asp Tyr Ile Thr Gly	
340 345 350	
ctg acc gtg tac acc cag agc agg agc atc agc agc gcc agg tac atc	1104
Leu Thr Val Tyr Thr Gln Ser Arg Ser Ile Ser Ser Ala Arg Tyr Ile	
355 360 365	
agg cac tgg gcc ggc cac cag atc agc tac cac agg gtg agc agg ggc	1152
Arg His Trp Ala Gly His Gln Ile Ser Tyr His Arg Val Ser Arg Gly	
370 375 380	
agc aac ctg cag cag atg tac ggc acc aac cag aac ctg cac agc acc	1200
Ser Asn Leu Gln Gln Met Tyr Gly Thr Asn Gln Asn Leu His Ser Thr	
385 390 395 400	
agc acc ttc gac ttc acc aac tac gac atc tac aag acc ctg agc aag	1248
Ser Thr Phe Asp Phe Thr Asn Tyr Asp Ile Tyr Lys Thr Leu Ser Lys	
405 410 415	
gac gcc gtg ctg ctg gac atc gtg tac cca ggc tac acc tac atc ttc	1296
Asp Ala Val Leu Leu Asp Ile Val Tyr Pro Gly Tyr Thr Tyr Ile Phe	
420 425 430	
ttc ggc atg cca gag gtg gag ttc ttc atg gtg aac cag ctg aac aac	1344

Phe	Gly	Met	Pro	Glu	Val	Glu	Phe	Phe	Met	Val	Asn	Gln	Leu	Asn	Asn		
		435					440					445					
acc	agg	aag	acc	ctg	aag	tac	aac	cca	gtg	agc	aag	gac	atc	atc	gct	1392	
Thr	Arg	Lys	Thr	Leu	Lys	Tyr	Asn	Pro	Val	Ser	Lys	Asp	Ile	Ile	Ala		
	450					455					460						
tct	aca	aga	gat	tct	gag	ctt	gag	ctt	cca	cca	gag	aca	tct	gat	cag	1440	
Ser	Thr	Arg	Asp	Ser	Glu	Leu	Glu	Leu	Pro	Pro	Glu	Thr	Ser	Asp	Gln		
	465					470					475				480		
cca	aat	tac	gag	tct	tac	tct	cat	aga	ctt	tgc	cat	att	aca	tct	att	1488	
Pro	Asn	Tyr	Glu	Ser	Tyr	Ser	His	Arg	Leu	Cys	His	Ile	Thr	Ser	Ile		
				485					490						495		
cca	gct	aca	ggt	aat	aca	aca	ggt	ctt	gtt	cca	ggt	ttc	tct	tgg	aca	1536	
Pro	Ala	Thr	Gly	Asn	Thr	Thr	Gly	Leu	Val	Pro	Val	Phe	Ser	Trp	Thr		
			500					505						510			
cat	aga	tct	gct	gat	ctt	aat	aat	aca	att	tac	tct	gat	aag	att	aca	1584	
His	Arg	Ser	Ala	Asp	Leu	Asn	Asn	Thr	Ile	Tyr	Ser	Asp	Lys	Ile	Thr		
		515					520					525					
cag	att	cca	gct	gtt	aag	tgc	tgg	gat	aat	ctt	cca	ttc	gtt	cca	gtt	1632	
Gln	Ile	Pro	Ala	Val	Lys	Cys	Trp	Asp	Asn	Leu	Pro	Phe	Val	Pro	Val		
	530					535					540						
gtt	aag	ggt	cca	ggt	cat	aca	ggt	ggt	gat	ctt	ctt	cag	tac	aat	aga	1680	
Val	Lys	Gly	Pro	Gly	His	Thr	Gly	Gly	Asp	Leu	Leu	Gln	Tyr	Asn	Arg		
	545				550					555					560		
tct	aca	ggt	tct	gtt	ggt	aca	ctt	ttc	ctt	gct	aga	tac	ggt	ctt	gct	1728	
Ser	Thr	Gly	Ser	Val	Gly	Thr	Leu	Phe	Leu	Ala	Arg	Tyr	Gly	Leu	Ala		
				565					570					575			
ctt	gag	aag	gct	ggt	aag	tac	aga	gtt	aga	ctt	aga	tac	gct	aca	gat	1776	
Leu	Glu	Lys	Ala	Gly	Lys	Tyr	Arg	Val	Arg	Leu	Arg	Tyr	Ala	Thr	Asp		
			580					585					590				
gct	gat	att	gtt	ctt	cat	gtt	aat	gat	gct	cag	att	cag	atg	cca	aag	1824	
Ala	Asp	Ile	Val	Leu	His	Val	Asn	Asp	Ala	Gln	Ile	Gln	Met	Pro	Lys		
		595					600					605					
aca	atg	aat	cca	ggt	gag	gat	ctt	aca	tct	aag	aca	ttc	aag	gtt	gct	1872	
Thr	Met	Asn	Pro	Gly	Glu	Asp	Leu	Thr	Ser	Lys	Thr	Phe	Lys	Val	Ala		
	610					615					620						
gat	gct	att	aca	aca	gtt	aat	ctt	gct	aca	gat	tct	tct	gtt	gct	gtt	1920	
Asp	Ala	Ile	Thr	Thr	Val	Asn	Leu	Ala	Thr	Asp	Ser	Ser	Val	Ala	Val		
	625				630					635					640		
aag	cat	aat	gtt	ggt	gag	gat	cca	aat	tct	aca	ctt	tct	ggt	att	gtt	1968	
Lys	His	Asn	Val	Gly	Glu	Asp	Pro	Asn	Ser	Thr	Leu	Ser	Gly	Ile	Val		
				645					650					655			
tac	gtt	gat	aga	att	gag	ttc	att	cca	gtt	gat	gag	aca	tac	gag	gct	2016	
Tyr	Val	Asp	Arg	Ile	Glu	Phe	Ile	Pro	Val	Asp	Glu	Thr	Tyr	Glu	Ala		

660

665

670

gag tga
Glu *

2022

<210> 64

<211> 673

<212> PRT

<213> *Bacillus thuringiensis* (mutated)

<400> 64

Met	Ser	Pro	Asn	Asn	Gln	Asn	Glu	Tyr	Glu	Ile	Ile	Asp	Ala	Thr	Pro
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Ser	Thr	Ser	Val	Ser	Asn	Asp	Ser	Asn	Arg	Tyr	Pro	Phe	Ala	Asn	Glu
			20				25					30			
Pro	Thr	Asn	Ala	Leu	Gln	Asn	Met	Asp	Tyr	Lys	Asp	Tyr	Leu	Lys	Met
		35				40					45				
Ser	Ala	Gly	Asn	Ala	Ser	Glu	Tyr	Pro	Gly	Ser	Pro	Glu	Val	Leu	Val
	50					55				60					
Ser	Gly	Gln	Asp	Ala	Ala	Lys	Ala	Ala	Ile	Asp	Ile	Val	Gly	Lys	Leu
65				70					75					80	
Leu	Ser	Gly	Leu	Gly	Val	Pro	Phe	Val	Gly	Pro	Ile	Val	Ser	Leu	Tyr
			85					90					95		
Thr	Gln	Leu	Ile	Asp	Ile	Leu	Trp	Pro	Ser	Gly	Glu	Lys	Ser	Gln	Trp
		100					105					110			
Glu	Ile	Phe	Met	Glu	Gln	Val	Glu	Glu	Leu	Ile	Asn	Gln	Lys	Ile	Ala
	115					120					125				
Glu	Tyr	Ala	Arg	Asn	Lys	Ala	Leu	Ser	Glu	Leu	Glu	Gly	Leu	Gly	Asn
	130				135					140					
Asn	Tyr	Gln	Leu	Tyr	Leu	Thr	Ala	Leu	Glu	Glu	Trp	Glu	Glu	Asn	Pro
145				150					155					160	
Phe	Arg	Arg	Gly	Phe	Arg	Arg	Gly	Ala	Leu	Arg	Asp	Val	Arg	Asn	Arg
			165				170						175		
Phe	Glu	Ile	Leu	Asp	Ser	Leu	Phe	Thr	Gln	Tyr	Met	Pro	Ser	Phe	Arg
		180					185					190			
Val	Thr	Asn	Phe	Glu	Val	Pro	Phe	Leu	Thr	Val	Tyr	Ala	Met	Ala	Ala
	195					200						205			
Asn	Leu	His	Leu	Leu	Leu	Leu	Lys	Asp	Ala	Ser	Ile	Phe	Gly	Glu	Glu
	210				215						220				
Trp	Gly	Trp	Ser	Thr	Thr	Thr	Ile	Asn	Asn	Tyr	Tyr	Asp	Arg	Gln	Met
225				230					235					240	
Lys	Leu	Thr	Ala	Glu	Tyr	Ser	Asp	His	Cys	Val	Lys	Trp	Tyr	Glu	Thr
			245					250					255		
Gly	Leu	Ala	Lys	Leu	Lys	Gly	Thr	Ser	Ala	Lys	Gln	Trp	Val	Asp	Tyr
		260					265						270		
Asn	Gln	Phe	Arg	Arg	Glu	Met	Thr	Leu	Ala	Val	Leu	Asp	Val	Val	Ala
	275					280						285			
Leu	Phe	Pro	Asn	Tyr	Asp	Thr	Arg	Thr	Tyr	Pro	Met	Glu	Thr	Lys	Ala
	290				295					300					
Gln	Leu	Thr	Arg	Glu	Val	Tyr	Thr	Asp	Pro	Leu	Gly	Ala	Val	Asn	Val
305				310					315					320	
Ser	Ser	Ile	Gly	Ser	Trp	Tyr	Asp	Lys	Ala	Pro	Ser	Phe	Gly	Val	Ile
			325					330					335		
Glu	Ser	Ser	Val	Ile	Arg	Pro	Pro	His	Val	Phe	Asp	Tyr	Ile	Thr	Gly
		340					345						350		

Leu Thr Val Tyr Thr Gln Ser Arg Ser Ile Ser Ser Ala Arg Tyr Ile
 355 360 365
 Arg His Trp Ala Gly His Gln Ile Ser Tyr His Arg Val Ser Arg Gly
 370 375 380
 Ser Asn Leu Gln Gln Met Tyr Gly Thr Asn Gln Asn Leu His Ser Thr
 385 390 395 400
 Ser Thr Phe Asp Phe Thr Asn Tyr Asp Ile Tyr Lys Thr Leu Ser Lys
 405 410 415
 Asp Ala Val Leu Leu Asp Ile Val Tyr Pro Gly Tyr Thr Tyr Ile Phe
 420 425 430
 Phe Gly Met Pro Glu Val Glu Phe Phe Met Val Asn Gln Leu Asn Asn
 435 440 445
 Thr Arg Lys Thr Leu Lys Tyr Asn Pro Val Ser Lys Asp Ile Ile Ala
 450 455 460
 Ser Thr Arg Asp Ser Glu Leu Glu Leu Pro Pro Glu Thr Ser Asp Gln
 465 470 475 480
 Pro Asn Tyr Glu Ser Tyr Ser His Arg Leu Cys His Ile Thr Ser Ile
 485 490 495
 Pro Ala Thr Gly Asn Thr Thr Gly Leu Val Pro Val Phe Ser Trp Thr
 500 505 510
 His Arg Ser Ala Asp Leu Asn Asn Thr Ile Tyr Ser Asp Lys Ile Thr
 515 520 525
 Gln Ile Pro Ala Val Lys Cys Trp Asp Asn Leu Pro Phe Val Pro Val
 530 535 540
 Val Lys Gly Pro Gly His Thr Gly Gly Asp Leu Leu Gln Tyr Asn Arg
 545 550 555 560
 Ser Thr Gly Ser Val Gly Thr Leu Phe Leu Ala Arg Tyr Gly Leu Ala
 565 570 575
 Leu Glu Lys Ala Gly Lys Tyr Arg Val Arg Leu Arg Tyr Ala Thr Asp
 580 585 590
 Ala Asp Ile Val Leu His Val Asn Asp Ala Gln Ile Gln Met Pro Lys
 595 600 605
 Thr Met Asn Pro Gly Glu Asp Leu Thr Ser Lys Thr Phe Lys Val Ala
 610 615 620
 Asp Ala Ile Thr Thr Val Asn Leu Ala Thr Asp Ser Ser Val Ala Val
 625 630 635 640
 Lys His Asn Val Gly Glu Asp Pro Asn Ser Thr Leu Ser Gly Ile Val
 645 650 655
 Tyr Val Asp Arg Ile Glu Phe Ile Pro Val Asp Glu Thr Tyr Glu Ala
 660 665 670
 Glu

<210> 65
 <211> 2022
 <212> DNA
 <213> Bacillus thuringiensis (mutated)

<220>
 <221> CDS
 <222> (1)...(2022)

<400> 65
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agc acc agc gtg agc aac gac agc aac cgc tac cca ttc gcc aac gag	96
Ser Thr Ser Val Ser Asn Asp Ser Asn Arg Tyr Pro Phe Ala Asn Glu	
20 25 30	
cca acc aac gcc ctc cag aac atg gac tac aag gac tac ctg aag atg	144
Pro Thr Asn Ala Leu Gln Asn Met Asp Tyr Lys Asp Tyr Leu Lys Met	
35 40 45	
agc gcc ggc aac gcc agc gag tac cca ggc agc cca gag gtg ctg gtg	192
Ser Ala Gly Asn Ala Ser Glu Tyr Pro Gly Ser Pro Glu Val Leu Val	
50 55 60	
agc ggc cag gac gcc gcc aag gcc gcc atc gac atc gtg ggc aag ctg	240
Ser Gly Gln Asp Ala Ala Lys Ala Ala Ile Asp Ile Val Gly Lys Leu	
65 70 75 80	
ctg agc ggc ctg ggc gtg cca ttc gtt ggc cca atc gtg agc ctg tac	288
Leu Ser Gly Leu Gly Val Pro Phe Val Gly Pro Ile Val Ser Leu Tyr	
85 90 95	
acc cag ctg atc gac atc ctg tgg cca agc ggc gag aag agc cag tgg	336
Thr Gln Leu Ile Asp Ile Leu Trp Pro Ser Gly Glu Lys Ser Gln Trp	
100 105 110	
gag atc ttc atg gag cag gtg gag gag ctg atc aac cag aag atc gcc	384
Glu Ile Phe Met Glu Gln Val Glu Glu Leu Ile Asn Gln Lys Ile Ala	
115 120 125	
gag tac gcc agg aac aag gcc ctg agc gag ctc gag ggc ctg ggc aac	432
Glu Tyr Ala Arg Asn Lys Ala Leu Ser Glu Leu Glu Gly Leu Gly Asn	
130 135 140	
aac tac cag ctg tac ctg acc gcc ctg gag gag tgg gag gag aac cca	480
Asn Tyr Gln Leu Tyr Leu Thr Ala Leu Glu Glu Trp Glu Glu Asn Pro	
145 150 155 160	
ttc agg agg ggc ttc agg agg ggc gcc ctg agg gac gtg agg aac agg	528
Phe Arg Arg Gly Phe Arg Arg Gly Ala Leu Arg Asp Val Arg Asn Arg	
165 170 175	
ttc gag atc ctg gac agc ctg ttc acc cag tac atg cct agc ttc agg	576
Phe Glu Ile Leu Asp Ser Leu Phe Thr Gln Tyr Met Pro Ser Phe Arg	
180 185 190	
gtg acc aac ttc gag gtg cca ttc ctg acc gtg tac gct atg gcc gcc	624
Val Thr Asn Phe Glu Val Pro Phe Leu Thr Val Tyr Ala Met Ala Ala	
195 200 205	
aac ctg cac ctg ctg ctg ctg aag gac gcc agc atc ttc ggc gag gag	672
Asn Leu His Leu Leu Leu Leu Lys Asp Ala Ser Ile Phe Gly Glu Glu	
210 215 220	
tgg ggc tgg agc acc acc acc atc aac aac tac tac gac agg cag atg	720
Trp Gly Trp Ser Thr Thr Thr Ile Asn Asn Tyr Tyr Asp Arg Gln Met	
225 230 235 240	

aag ctg acc gcc gag tac agc gac cac tgc gtg aag tgg tac gag acc	768
Lys Leu Thr Ala Glu Tyr Ser Asp His Cys Val Lys Trp Tyr Glu Thr	
245 250 255	
ggc ctg gcc aag ctg aag ggc acc agc gcc aag cag tgg gtg gac tac	816
Gly Leu Ala Lys Leu Lys Gly Thr Ser Ala Lys Gln Trp Val Asp Tyr	
260 265 270	
aac cag ttc agg agg gag atg acc ctg gcc gtg ctg gac gtg gtg gcc	864
Asn Gln Phe Arg Arg Glu Met Thr Leu Ala Val Leu Asp Val Val Ala	
275 280 285	
ctg ttc cca aac tac gac acc agg acc tac cca atg gag acc aag gcc	912
Leu Phe Pro Asn Tyr Asp Thr Arg Thr Tyr Pro Met Glu Thr Lys Ala	
290 295 300	
cag ctg acc agg gag gtg tac acc gac cca ctg ggc gcc gtg aac gtg	960
Gln Leu Thr Arg Glu Val Tyr Thr Asp Pro Leu Gly Ala Val Asn Val	
305 310 315 320	
agc agc atc ggc agc tgg tac gac aag gcc cca agc ttc ggc gtg atc	1008
Ser Ser Ile Gly Ser Trp Tyr Asp Lys Ala Pro Ser Phe Gly Val Ile	
325 330 335	
gag agc agc gtg atc agg cca cca cac gtg ttc gac tac atc acc ggc	1056
Glu Ser Ser Val Ile Arg Pro Pro His Val Phe Asp Tyr Ile Thr Gly	
340 345 350	
ctg acc gtg tac acc cag agc agg agc atc agc agc gcc aga tac atc	1104
Leu Thr Val Tyr Thr Gln Ser Arg Ser Ile Ser Ser Ala Arg Tyr Ile	
355 360 365	
agg cac tgg gcc ggc cac cag atc agc tac cac agg gtg agc agg ggc	1152
Arg His Trp Ala Gly His Gln Ile Ser Tyr His Arg Val Ser Arg Gly	
370 375 380	
agc aac ctg cag cag atg tac ggc acc aac cag aac ctg cac agc acc	1200
Ser Asn Leu Gln Gln Met Tyr Gly Thr Asn Gln Asn Leu His Ser Thr	
385 390 395 400	
agc acc ttc gac ttc acc aac tac gac atc tac aag acc ctg agc aag	1248
Ser Thr Phe Asp Phe Thr Asn Tyr Asp Ile Tyr Lys Thr Leu Ser Lys	
405 410 415	
gac gcc gtg ctg ctg gac atc gtg tac cca ggc tac acc tac atc ttc	1296
Asp Ala Val Leu Leu Asp Ile Val Tyr Pro Gly Tyr Thr Tyr Ile Phe	
420 425 430	
ttc ggc atg cca gag gtg gag ttc ttc atg gtg aac cag ctg aac aac	1344
Phe Gly Met Pro Glu Val Glu Phe Phe Met Val Asn Gln Leu Asn Asn	
435 440 445	
acc agg aag acc ctg aag tac aac cca gtg agc aag gac atc atc gct	1392
Thr Arg Lys Thr Leu Lys Tyr Asn Pro Val Ser Lys Asp Ile Ile Ala	
450 455 460	
tct aca aga gat tct gag ctt gag ctt cca cca gag aca tct gat cag	1440

Ser Thr Arg Asp Ser Glu Leu Glu Leu Pro Pro Glu Thr Ser Asp Gln	
465 470 475 480	
cca aat tac gag tct tac tct cat aga ctt tgc cat att aca tct att	1488
Pro Asn Tyr Glu Ser Tyr Ser His Arg Leu Cys His Ile Thr Ser Ile	
485 490 495	
cca gct aca ggc aat act aca ggt ctt gtt cca gtt ttc tct tgg aca	1536
Pro Ala Thr Gly Asn Thr Thr Gly Leu Val Pro Val Phe Ser Trp Thr	
500 505 510	
cat aga tct gct gat ctt aat aat act atc tac tct gat aag att aca	1584
His Arg Ser Ala Asp Leu Asn Asn Thr Ile Tyr Ser Asp Lys Ile Thr	
515 520 525	
cag att cca gct gtt aag tgc tgg gat aat ctt cca ttc gtt cca gtt	1632
Gln Ile Pro Ala Val Lys Cys Trp Asp Asn Leu Pro Phe Val Pro Val	
530 535 540	
gtt aag ggc cca ggt cat aca ggt ggt gat ctt ctt cag tac aat aga	1680
Val Lys Gly Pro Gly His Thr Gly Gly Asp Leu Leu Gln Tyr Asn Arg	
545 550 555 560	
tct aca ggt tct gtt ggt aca ctt ttc ctt gct aga tac ggt ctt gct	1728
Ser Thr Gly Ser Val Gly Thr Leu Phe Leu Ala Arg Tyr Gly Leu Ala	
565 570 575	
ctt gag aag gct ggt aag tac aga gtt aga ctt aga tac gct aca gat	1776
Leu Glu Lys Ala Gly Lys Tyr Arg Val Arg Leu Arg Tyr Ala Thr Asp	
580 585 590	
gct gat att gtt ctt cat gtt aat gat gct cag att cag atg cca aag	1824
Ala Asp Ile Val Leu His Val Asn Asp Ala Gln Ile Gln Met Pro Lys	
595 600 605	
aca atg aat cca ggc gag gat ctt aca tct aag aca ttc aag gtt gct	1872
Thr Met Asn Pro Gly Glu Asp Leu Thr Ser Lys Thr Phe Lys Val Ala	
610 615 620	
gat gct att aca aca gtt aat ctt gct aca gat tct tct gtt gct gtt	1920
Asp Ala Ile Thr Thr Val Asn Leu Ala Thr Asp Ser Ser Val Ala Val	
625 630 635 640	
aag cac aat gtt ggc gag gac cca aat tct aca ctt tct ggt att gtt	1968
Lys His Asn Val Gly Glu Asp Pro Asn Ser Thr Leu Ser Gly Ile Val	
645 650 655	
tac gtt gat agg att gag ttc att cca gtt gat gag aca tac gag gct	2016
Tyr Val Asp Arg Ile Glu Phe Ile Pro Val Asp Glu Thr Tyr Glu Ala	
660 665 670	
gag tga	2022
Glu *	

<210> 66

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 Phe Gly Met Pro Glu Val Glu Phe Phe Met Val Asn Gln Leu Asn Asn
 435 440 445
 Thr Arg Lys Thr Leu Lys Tyr Asn Pro Val Ser Lys Asp Ile Ile Ala
 450 455 460
 Ser Thr Arg Asp Ser Glu Leu Glu Leu Pro Pro Glu Thr Ser Asp Gln
 465 470 475 480
 Pro Asn Tyr Glu Ser Tyr Ser His Arg Leu Cys His Ile Thr Ser Ile
 485 490 495
 Pro Ala Thr Gly Asn Thr Thr Gly Leu Val Pro Val Phe Ser Trp Thr
 500 505 510
 His Arg Ser Ala Asp Leu Asn Asn Thr Ile Tyr Ser Asp Lys Ile Thr
 515 520 525
 Gln Ile Pro Ala Val Lys Cys Trp Asp Asn Leu Pro Phe Val Pro Val
 530 535 540
 Val Lys Gly Pro Gly His Thr Gly Gly Asp Leu Leu Gln Tyr Asn Arg
 545 550 555 560
 Ser Thr Gly Ser Val Gly Thr Leu Phe Leu Ala Arg Tyr Gly Leu Ala
 565 570 575
 Leu Glu Lys Ala Gly Lys Tyr Arg Val Arg Leu Arg Tyr Ala Thr Asp
 580 585 590
 Ala Asp Ile Val Leu His Val Asn Asp Ala Gln Ile Gln Met Pro Lys
 595 600 605
 Thr Met Asn Pro Gly Glu Asp Leu Thr Ser Lys Thr Phe Lys Val Ala
 610 615 620
 Asp Ala Ile Thr Thr Val Asn Leu Ala Thr Asp Ser Ser Val Ala Val
 625 630 635 640
 Lys His Asn Val Gly Glu Asp Pro Asn Ser Thr Leu Ser Gly Ile Val
 645 650 655
 Tyr Val Asp Arg Ile Glu Phe Ile Pro Val Asp Glu Thr Tyr Glu Ala
 660 665 670
 Glu

<210> 67
 <211> 2022
 <212> DNA
 <213> *Bacillus thuringiensis* (mutated)

<220>
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 tct act tct gta tcc aat gat tct aac aga tac cct ttt gcg aat gag 96
 Ser Thr Ser Val Ser Asn Asp Ser Asn Arg Tyr Pro Phe Ala Asn Glu
 20 25 30

 cca aca aat gcg cta caa aat atg gat tat aaa gat tat tta aaa atg 144
 Pro Thr Asn Ala Leu Gln Asn Met Asp Tyr Lys Asp Tyr Leu Lys Met
 35 40 45

tct gcg gga aat gct agt gaa tac cct ggt tca cct gaa gta ctt gtt	192
Ser Ala Gly Asn Ala Ser Glu Tyr Pro Gly Ser Pro Glu Val Leu Val	
50 55 60	
agc gga caa gat gca gct aag gcc gca att gat ata gta ggt aaa tta	240
Ser Gly Gln Asp Ala Ala Lys Ala Ala Ile Asp Ile Val Gly Lys Leu	
65 70 75 80	
cta tca ggt tta ggg gtc cca ttt gtt ggg ccg ata gtg agt ctt tat	288
Leu Ser Gly Leu Gly Val Pro Phe Val Gly Pro Ile Val Ser Leu Tyr	
85 90 95	
act caa ctt att gat att ctg tgg cct tca ggg gaa aag agt caa tgg	336
Thr Gln Leu Ile Asp Ile Leu Trp Pro Ser Gly Glu Lys Ser Gln Trp	
100 105 110	
gaa att ttt atg gaa caa gta gaa gaa ctc att aat caa aaa ata gca	384
Glu Ile Phe Met Glu Gln Val Glu Glu Leu Ile Asn Gln Lys Ile Ala	
115 120 125	
gaa tat gca agg aat aaa gcg ctt tcg gaa tta gaa gga tta ggt aat	432
Glu Tyr Ala Arg Asn Lys Ala Leu Ser Glu Leu Glu Gly Leu Gly Asn	
130 135 140	
aat tac caa tta tat cta act gcg ctt gaa gaa tgg gaa gaa aat cca	480
Asn Tyr Gln Leu Tyr Leu Thr Ala Leu Glu Glu Trp Glu Glu Asn Pro	
145 150 155 160	
ttt cga cga ggt ttt cga cga ggt gcc tta cga gat gtg cga aat cga	528
Phe Arg Arg Gly Phe Arg Arg Gly Ala Leu Arg Asp Val Arg Asn Arg	
165 170 175	
ttt gaa atc ctg gat agt tta ttt acg caa tat atg cca tct ttt aga	576
Phe Glu Ile Leu Asp Ser Leu Phe Thr Gln Tyr Met Pro Ser Phe Arg	
180 185 190	
gtg aca aat ttt gaa gta cca ttc ctt act gta tat gca atg gca gcc	624
Val Thr Asn Phe Glu Val Pro Phe Leu Thr Val Tyr Ala Met Ala Ala	
195 200 205	
aac ctt cat tta ctg tta tta aag gac gcg tca att ttt gga gaa gaa	672
Asn Leu His Leu Leu Leu Leu Lys Asp Ala Ser Ile Phe Gly Glu Glu	
210 215 220	
tgg gga tgg tca aca act act att aat aac tat tat gat cgt caa atg	720
Trp Gly Trp Ser Thr Thr Thr Ile Asn Asn Tyr Tyr Asp Arg Gln Met	
225 230 235 240	
aaa ctt act gca gaa tat tct gat cac tgt gta aag tgg tat gaa act	768
Lys Leu Thr Ala Glu Tyr Ser Asp His Cys Val Lys Trp Tyr Glu Thr	
245 250 255	
ggg tta gca aaa tta aaa ggc acg agc gct aaa caa tgg gtt gac tat	816
Gly Leu Ala Lys Leu Lys Gly Thr Ser Ala Lys Gln Trp Val Asp Tyr	
260 265 270	

aac caa ttc cgt aga gaa atg aca ctg gcg gtt tta gat gtt gtt gca	864
Asn Gln Phe Arg Arg Glu Met Thr Leu Ala Val Leu Asp Val Val Ala	
275 280 285	
tta ttc cca aat tat gac aca cgc acg tac cca atg gaa acg aaa gca	912
Leu Phe Pro Asn Tyr Asp Thr Arg Thr Tyr Pro Met Glu Thr Lys Ala	
290 295 300	
caa cta aca agg gaa gta tat aca gat cca ctg ggc gcg gta aac gtg	960
Gln Leu Thr Arg Glu Val Tyr Thr Asp Pro Leu Gly Ala Val Asn Val	
305 310 315 320	
tct tca att ggt tcc tgg tat gac aaa gca cct tct ttc gga gtg ata	1008
Ser Ser Ile Gly Ser Trp Tyr Asp Lys Ala Pro Ser Phe Gly Val Ile	
325 330 335	
gaa tca tcc gtt att cga cca ccc cat gta ttt gat tat ata acg gga	1056
Glu Ser Ser Val Ile Arg Pro Pro His Val Phe Asp Tyr Ile Thr Gly	
340 345 350	
ctc aca gtg tat aca caa tca aga agc att tct tcc gct cgc tat ata	1104
Leu Thr Val Tyr Thr Gln Ser Arg Ser Ile Ser Ser Ala Arg Tyr Ile	
355 360 365	
aga cat tgg gct ggt cat caa ata agc tac cat cgt gtc agt agg ggt	1152
Arg His Trp Ala Gly His Gln Ile Ser Tyr His Arg Val Ser Arg Gly	
370 375 380	
agt aat ctt caa caa atg tat gga act aat caa aat cta cac agc act	1200
Ser Asn Leu Gln Gln Met Tyr Gly Thr Asn Gln Asn Leu His Ser Thr	
385 390 395 400	
agt acc ttt gat ttt acg aat tat gat att tac aag act cta tca aag	1248
Ser Thr Phe Asp Phe Thr Asn Tyr Asp Ile Tyr Lys Thr Leu Ser Lys	
405 410 415	
gat gca gta ctc ctt gat att gtt tac cct ggt tat acg tat ata ttt	1296
Asp Ala Val Leu Leu Asp Ile Val Tyr Pro Gly Tyr Thr Tyr Ile Phe	
420 425 430	
ttt gga atg cca gaa gtc gag ttt ttc atg gta aac caa ttg aat aat	1344
Phe Gly Met Pro Glu Val Glu Phe Phe Met Val Asn Gln Leu Asn Asn	
435 440 445	
acc aga aag acg tta aag tat aat cca gtt tcc aaa gat att ata gcg	1392
Thr Arg Lys Thr Leu Lys Tyr Asn Pro Val Ser Lys Asp Ile Ile Ala	
450 455 460	
agt aca aga gat tcg gaa tta gaa tta cct cca gaa act tca gat caa	1440
Ser Thr Arg Asp Ser Glu Leu Glu Leu Pro Pro Glu Thr Ser Asp Gln	
465 470 475 480	
cca aat tat gag tca tat agc cat aga tta tgt cat atc aca agt att	1488
Pro Asn Tyr Glu Ser Tyr Ser His Arg Leu Cys His Ile Thr Ser Ile	
485 490 495	
ccc gcg acg ggt aac act acc gga tta gta cct gta ttt tct tgg aca	1536

Pro	Ala	Thr	Gly	Asn	Thr	Thr	Gly	Leu	Val	Pro	Val	Phe	Ser	Trp	Thr		
			500					505					510				
cat	cga	agt	gca	gat	tta	aac	aat	aca	ata	tat	tca	gat	aaa	atc	act	1584	
His	Arg	Ser	Ala	Asp	Leu	Asn	Asn	Thr	Ile	Tyr	Ser	Asp	Lys	Ile	Thr		
		515					520					525					
caa	att	ccg	gcc	gtt	aaa	tgt	tgg	gat	aat	tta	ccg	ttt	gtt	cca	gtg	1632	
Gln	Ile	Pro	Ala	Val	Lys	Cys	Trp	Asp	Asn	Leu	Pro	Phe	Val	Pro	Val		
	530					535					540						
gta	aaa	gga	cca	gga	cat	aca	gga	ggg	gat	tta	tta	cag	tat	aat	aga	1680	
Val	Lys	Gly	Pro	Gly	His	Thr	Gly	Gly	Asp	Leu	Leu	Gln	Tyr	Asn	Arg		
545					550				555					560			
agt	act	ggg	tct	gta	gga	acc	tta	ttt	cta	gct	cga	tat	ggc	cta	gca	1728	
Ser	Thr	Gly	Ser	Val	Gly	Thr	Leu	Phe	Leu	Ala	Arg	Tyr	Gly	Leu	Ala		
			565					570						575			
tta	gaa	aaa	gca	ggg	aaa	tat	cgt	gta	aga	ctg	aga	tat	gct	act	gat	1776	
Leu	Glu	Lys	Ala	Gly	Lys	Tyr	Arg	Val	Arg	Leu	Arg	Tyr	Ala	Thr	Asp		
		580					585						590				
gca	gat	att	gta	ttg	cat	gta	aac	gat	gct	cag	att	cag	atg	cca	aaa	1824	
Ala	Asp	Ile	Val	Leu	His	Val	Asn	Asp	Ala	Gln	Ile	Gln	Met	Pro	Lys		
	595					600						605					
aca	atg	aac	cca	ggg	gag	gat	ctg	aca	tct	aaa	act	ttt	aaa	gtt	gca	1872	
Thr	Met	Asn	Pro	Gly	Glu	Asp	Leu	Thr	Ser	Lys	Thr	Phe	Lys	Val	Ala		
	610					615					620						
gat	gct	atc	aca	aca	gta	aat	tta	gca	aca	gat	agt	tcg	gta	gca	gtg	1920	
Asp	Ala	Ile	Thr	Thr	Val	Asn	Leu	Ala	Thr	Asp	Ser	Ser	Val	Ala	Val		
625					630					635					640		
aaa	cat	aat	tta	ggg	gaa	gac	cct	aat	tca	aca	tta	tct	ggg	ata	gtt	1968	
Lys	His	Asn	Leu	Gly	Glu	Asp	Pro	Asn	Ser	Thr	Leu	Ser	Gly	Ile	Val		
			645					650					655				
tac	gtt	gac	cga	atc	gaa	ttc	atc	cca	gta	gat	gag	aca	tat	gaa	gcg	2016	
Tyr	Val	Asp	Arg	Ile	Glu	Phe	Ile	Pro	Val	Asp	Glu	Thr	Tyr	Glu	Ala		
		660					665						670				
gaa	taa															2022	
Glu	*																

<210> 68
 <211> 673
 <212> PRT
 <213> Bacillus thuringiensis (mutated)

<400> 68
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 Ser Thr Ser Val Ser Asn Asp Ser Asn Arg Tyr Pro Phe Ala Asn Glu

RTA01/2138018v1

Pro	Asn	Tyr	Glu	Ser	Tyr	Ser	His	Arg	Leu	Cys	His	Ile	Thr	Ser	Ile	
				485					490						495	
Pro	Ala	Thr	Gly	Asn	Thr	Thr	Gly	Leu	Val	Pro	Val	Phe	Ser	Trp	Thr	
			500					505						510		
His	Arg	Ser	Ala	Asp	Leu	Asn	Asn	Thr	Ile	Tyr	Ser	Asp	Lys	Ile	Thr	
		515					520					525				
Gln	Ile	Pro	Ala	Val	Lys	Cys	Trp	Asp	Asn	Leu	Pro	Phe	Val	Pro	Val	
	530					535					540					
Val	Lys	Gly	Pro	Gly	His	Thr	Gly	Gly	Asp	Leu	Leu	Gln	Tyr	Asn	Arg	
545					550					555					560	
Ser	Thr	Gly	Ser	Val	Gly	Thr	Leu	Phe	Leu	Ala	Arg	Tyr	Gly	Leu	Ala	
				565					570						575	
Leu	Glu	Lys	Ala	Gly	Lys	Tyr	Arg	Val	Arg	Leu	Arg	Tyr	Ala	Thr	Asp	
			580					585						590		
Ala	Asp	Ile	Val	Leu	His	Val	Asn	Asp	Ala	Gln	Ile	Gln	Met	Pro	Lys	
	595						600					605				
Thr	Met	Asn	Pro	Gly	Glu	Asp	Leu	Thr	Ser	Lys	Thr	Phe	Lys	Val	Ala	
	610					615						620				
Asp	Ala	Ile	Thr	Thr	Val	Asn	Leu	Ala	Thr	Asp	Ser	Ser	Val	Ala	Val	
625					630					635					640	
Lys	His	Asn	Leu	Gly	Glu	Asp	Pro	Asn	Ser	Thr	Leu	Ser	Gly	Ile	Val	
				645					650					655		
Tyr	Val	Asp	Arg	Ile	Glu	Phe	Ile	Pro	Val	Asp	Glu	Thr	Tyr	Glu	Ala	
			660					665						670		
Glu																

<210> 69
 <211> 2022
 <212> DNA
 <213> *Bacillus thuringiensis* (mutated)

<220>
 <221> CDS
 <222> (1)...(2022)

<400> 69																
atg	agt	cca	aat	aat	caa	aat	gaa	tat	gaa	att	ata	gat	gcg	aca	cct	48
Met	Ser	Pro	Asn	Asn	Gln	Asn	Glu	Tyr	Glu	Ile	Ile	Asp	Ala	Thr	Pro	
1				5					10					15		
tct	act	tct	gta	tcc	aat	gat	tct	aac	aga	tac	cct	ttt	gcg	aat	gag	96
Ser	Thr	Ser	Val	Ser	Asn	Asp	Ser	Asn	Arg	Tyr	Pro	Phe	Ala	Asn	Glu	
			20					25					30			
cca	aca	aat	gcg	cta	caa	aat	atg	gat	tat	aaa	gat	tat	tta	aaa	atg	144
Pro	Thr	Asn	Ala	Leu	Gln	Asn	Met	Asp	Tyr	Lys	Asp	Tyr	Leu	Lys	Met	
		35					40				45					
tct	gcg	gga	aat	gct	agt	gaa	tac	cct	ggt	tca	cct	gaa	gta	ctt	gtt	192
Ser	Ala	Gly	Asn	Ala	Ser	Glu	Tyr	Pro	Gly	Ser	Pro	Glu	Val	Leu	Val	
	50					55					60					
agc	gga	caa	gat	gca	gct	aag	gcc	gca	att	gat	ata	gta	ggt	aaa	tta	240
Ser	Gly	Gln	Asp	Ala	Ala	Lys	Ala	Ala	Ile	Asp	Ile	Val	Gly	Lys	Leu	
	65					70				75					80	

cta tca ggt tta ggg gtc cca ttt gtt ggg ccg ata gtg agt ctt tat	288
Leu Ser Gly Leu Gly Val Pro Phe Val Gly Pro Ile Val Ser Leu Tyr	
85 90 95	
act caa ctt att gat att ctg tgg cct tca ggg gaa aag agt caa tgg	336
Thr Gln Leu Ile Asp Ile Leu Trp Pro Ser Gly Glu Lys Ser Gln Trp	
100 105 110	
gaa att ttt atg gaa caa gta gaa gaa ctc att aat caa aaa ata gca	384
Glu Ile Phe Met Glu Gln Val Glu Glu Leu Ile Asn Gln Lys Ile Ala	
115 120 125	
gaa tat gca agg aat aaa gcg ctt tcg gaa tta gaa gga tta ggt aat	432
Glu Tyr Ala Arg Asn Lys Ala Leu Ser Glu Leu Glu Gly Leu Gly Asn	
130 135 140	
aat tac caa tta tat cta act gcg ctt gaa gaa tgg gaa gaa aat cca	480
Asn Tyr Gln Leu Tyr Leu Thr Ala Leu Glu Glu Trp Glu Glu Asn Pro	
145 150 155 160	
aat ggt tca aga aat ggt tcc cgg gcc tta cga gat gtg cga aat cga	528
Asn Gly Ser Arg Asn Gly Ser Arg Ala Leu Arg Asp Val Arg Asn Arg	
165 170 175	
ttt gaa atc ctg gat agt tta ttt acg caa tat atg cca tct ttt aga	576
Phe Glu Ile Leu Asp Ser Leu Phe Thr Gln Tyr Met Pro Ser Phe Arg	
180 185 190	
gtg aca aat ttt gaa gta cca ttc ctt act gta tat gca atg gca gcc	624
Val Thr Asn Phe Glu Val Pro Phe Leu Thr Val Tyr Ala Met Ala Ala	
195 200 205	
aac ctt cat tta ctg tta tta aag gac gcg tca att ttt gga gaa gaa	672
Asn Leu His Leu Leu Leu Leu Lys Asp Ala Ser Ile Phe Gly Glu Glu	
210 215 220	
tgg gga tgg tca aca act act att aat aac tat tat gat cgt caa atg	720
Trp Gly Trp Ser Thr Thr Thr Ile Asn Asn Tyr Tyr Asp Arg Gln Met	
225 230 235 240	
aaa ctt act gca gaa tat tct gat cac tgt gta aag tgg tat gaa act	768
Lys Leu Thr Ala Glu Tyr Ser Asp His Cys Val Lys Trp Tyr Glu Thr	
245 250 255	
ggg tta gca aaa tta aaa ggc acg agc gct aaa caa tgg gtt gac tat	816
Gly Leu Ala Lys Leu Lys Gly Thr Ser Ala Lys Gln Trp Val Asp Tyr	
260 265 270	
aac caa ttc cgt aga gaa atg aca ctg gcg gtt tta gat gtt gtt gca	864
Asn Gln Phe Arg Arg Glu Met Thr Leu Ala Val Leu Asp Val Val Ala	
275 280 285	
tta ttc cca aat tat gac aca cgc acg tac cca atg gaa acg aaa gca	912
Leu Phe Pro Asn Tyr Asp Thr Arg Thr Tyr Pro Met Glu Thr Lys Ala	
290 295 300	

caa cta aca agg gaa gta tat aca gat cca ctg ggc gcg gta aac gtg	960
Gln Leu Thr Arg Glu Val Tyr Thr Asp Pro Leu Gly Ala Val Asn Val	
305 310 315 320	
tct tca att ggt tcc tgg tat gac aaa gca cct tct ttc gga gtg ata	1008
Ser Ser Ile Gly Ser Trp Tyr Asp Lys Ala Pro Ser Phe Gly Val Ile	
325 330 335	
gaa tca tcc gtt att cga cca ccc cat gta ttt gat tat ata acg gga	1056
Glu Ser Ser Val Ile Arg Pro Pro His Val Phe Asp Tyr Ile Thr Gly	
340 345 350	
ctc aca gtg tat aca caa tca aga agc att tct tcc gct cgc tat ata	1104
Leu Thr Val Tyr Thr Gln Ser Arg Ser Ile Ser Ser Ala Arg Tyr Ile	
355 360 365	
aga cat tgg gct ggt cat caa ata agc tac cat cgt gtc agt agg ggt	1152
Arg His Trp Ala Gly His Gln Ile Ser Tyr His Arg Val Ser Arg Gly	
370 375 380	
agt aat ctt caa caa atg tat gga act aat caa aat cta cac agc act	1200
Ser Asn Leu Gln Gln Met Tyr Gly Thr Asn Gln Asn Leu His Ser Thr	
385 390 395 400	
agt acc ttt gat ttt acg aat tat gat att tac aag act cta tca aag	1248
Ser Thr Phe Asp Phe Thr Asn Tyr Asp Ile Tyr Lys Thr Leu Ser Lys	
405 410 415	
gat gca gta ctc ctt gat att gtt tac cct ggt tat acg tat ata ttt	1296
Asp Ala Val Leu Leu Asp Ile Val Tyr Pro Gly Tyr Thr Tyr Ile Phe	
420 425 430	
ttt gga atg cca gaa gtc gag ttt ttc atg gta aac caa ttg aat aat	1344
Phe Gly Met Pro Glu Val Glu Phe Phe Met Val Asn Gln Leu Asn Asn	
435 440 445	
acc aga aag acg tta aag tat aat cca gtt tcc aaa gat att ata gcg	1392
Thr Arg Lys Thr Leu Lys Tyr Asn Pro Val Ser Lys Asp Ile Ile Ala	
450 455 460	
agt aca aga gat tcg gaa tta gaa tta cct cca gaa act tca gat caa	1440
Ser Thr Arg Asp Ser Glu Leu Glu Leu Pro Pro Glu Thr Ser Asp Gln	
465 470 475 480	
cca aat tat gag tca tat agc cat aga tta tgt cat atc aca agt att	1488
Pro Asn Tyr Glu Ser Tyr Ser His Arg Leu Cys His Ile Thr Ser Ile	
485 490 495	
ccc gcg acg ggt aac act acc gga tta gta cct gta ttt tct tgg aca	1536
Pro Ala Thr Gly Asn Thr Thr Gly Leu Val Pro Val Phe Ser Trp Thr	
500 505 510	
cat cga agt gca gat tta aac aat aca ata tat tca gat aaa atc act	1584
His Arg Ser Ala Asp Leu Asn Asn Thr Ile Tyr Ser Asp Lys Ile Thr	
515 520 525	
caa att ccg gcc gtt aaa tgt tgg gat aat tta ccg ttt gtt cca gtg	1632

Gln Ile Pro Ala Val Lys Cys Trp Asp Asn Leu Pro Phe Val Pro Val	
530 535 540	
gta aaa gga cca gga cat aca gga ggg gat tta tta cag tat aat aga	1680
Val Lys Gly Pro Gly His Thr Gly Gly Asp Leu Leu Gln Tyr Asn Arg	
545 550 555 560	
agt act ggt tct gta gga acc tta ttt cta gct cga tat ggc cta gca	1728
Ser Thr Gly Ser Val Gly Thr Leu Phe Leu Ala Arg Tyr Gly Leu Ala	
565 570 575	
tta gaa aaa gca ggg aaa tat cgt gta aga ctg aga tat gct act gat	1776
Leu Glu Lys Ala Gly Lys Tyr Arg Val Arg Leu Arg Tyr Ala Thr Asp	
580 585 590	
gca gat att gta ttg cat gta aac gat gct cag att cag atg cca aaa	1824
Ala Asp Ile Val Leu His Val Asn Asp Ala Gln Ile Gln Met Pro Lys	
595 600 605	
aca atg aac cca ggt gag gat ctg aca tct aaa act ttt aaa gtt gca	1872
Thr Met Asn Pro Gly Glu Asp Leu Thr Ser Lys Thr Phe Lys Val Ala	
610 615 620	
gat gct atc aca aca gta aat tta gca aca gat agt tcg gta gca gtg	1920
Asp Ala Ile Thr Thr Val Asn Leu Ala Thr Asp Ser Ser Val Ala Val	
625 630 635 640	
aaa cat aat tta ggt gaa gac cct aat tca aca tta tct ggt ata gtt	1968
Lys His Asn Leu Gly Glu Asp Pro Asn Ser Thr Leu Ser Gly Ile Val	
645 650 655	
tac gtt gac cga atc gaa ttc atc cca gta gat gag aca tat gaa gcg	2016
Tyr Val Asp Arg Ile Glu Phe Ile Pro Val Asp Glu Thr Tyr Glu Ala	
660 665 670	
gaa taa	2022
Glu *	

<210> 70
 <211> 673
 <212> PRT
 <213> Bacillus thuringiensis (mutated)

<400> 70
 Met Ser Pro Asn Asn Gln Asn Glu Tyr Glu Ile Ile Asp Ala Thr Pro
 1 5 10 15
 Ser Thr Ser Val Ser Asn Asp Ser Asn Arg Tyr Pro Phe Ala Asn Glu
 20 25 30
 Pro Thr Asn Ala Leu Gln Asn Met Asp Tyr Lys Asp Tyr Leu Lys Met
 35 40 45
 Ser Ala Gly Asn Ala Ser Glu Tyr Pro Gly Ser Pro Glu Val Leu Val
 50 55 60
 Ser Gly Gln Asp Ala Ala Lys Ala Ala Ile Asp Ile Val Gly Lys Leu
 65 70 75 80
 Leu Ser Gly Leu Gly Val Pro Phe Val Gly Pro Ile Val Ser Leu Tyr

Val Lys Gly Pro Gly His Thr Gly Gly Asp Leu Leu Gln Tyr Asn Arg
545 550 555 560
Ser Thr Gly Ser Val Gly Thr Leu Phe Leu Ala Arg Tyr Gly Leu Ala
565 570 575
Leu Glu Lys Ala Gly Lys Tyr Arg Val Arg Leu Arg Tyr Ala Thr Asp
580 585 590
Ala Asp Ile Val Leu His Val Asn Asp Ala Gln Ile Gln Met Pro Lys
595 600 605
Thr Met Asn Pro Gly Glu Asp Leu Thr Ser Lys Thr Phe Lys Val Ala
610 615 620
Asp Ala Ile Thr Thr Val Asn Leu Ala Thr Asp Ser Ser Val Ala Val
625 630 635 640
Lys His Asn Leu Gly Glu Asp Pro Asn Ser Thr Leu Ser Gly Ile Val
645 650 655
Tyr Val Asp Arg Ile Glu Phe Ile Pro Val Asp Glu Thr Tyr Glu Ala
660 665 670
Glu

<210> 71
<211> 2028
<212> DNA
<213> Bacillus thuringiensis (mutated)

<220>
<221> CDS
<222> (1)...(2028)

<400> 71
atg agt cca aat aat caa aat gaa tat gaa att ata gat gcg aca cct 48
Met Ser Pro Asn Asn Gln Asn Glu Tyr Glu Ile Ile Asp Ala Thr Pro
1 5 10 15
tct act tct gta tcc aat gat tct aac aga tac cct ttt gcg aat gag 96
Ser Thr Ser Val Ser Asn Asp Ser Asn Arg Tyr Pro Phe Ala Asn Glu
20 25 30
cca aca aat gcg cta caa aat atg gat tat aaa gat tat tta aaa atg 144
Pro Thr Asn Ala Leu Gln Asn Met Asp Tyr Lys Asp Tyr Leu Lys Met
35 40 45
tct gcg gga aat gct agt gaa tac cct ggt tca cct gaa gta ctt gtt 192
Ser Ala Ser Glu Tyr Pro Gly Ser Pro Glu Val Leu Val
50 55 60
agc gga caa gat gca gct aag gcc gca att gat ata gta ggt aaa tta 240
Ser Gly Gln Asp Ala Ala Lys Ala Ala Ile Asp Ile Val Gly Lys Leu
65 70 75 80
cta tca ggt tta ggg gtc cca ttt gtt ggg ccg ata gtg agt ctt tat 288
Leu Ser Gly Leu Gly Val Pro Phe Val Gly Pro Ile Val Ser Leu Tyr
85 90 95
act caa ctt att gat att ctg tgg cct tca ggg gaa aag agt caa tgg 336
Thr Gln Leu Ile Asp Ile Leu Trp Pro Ser Gly Glu Lys Ser Gln Trp
100 105 110

gaa att ttt atg gaa caa gta gaa gaa ctc att aat caa aaa ata gca	384
Glu Ile Phe Met Glu Gln Val Glu Glu Leu Ile Asn Gln Lys Ile Ala	
115 120 125	
gaa tat gca agg aat aaa gcg ctt tcg gaa tta gaa gga tta ggt aat	432
Glu Tyr Ala Arg Asn Lys Ala Leu Ser Glu Leu Glu Gly Leu Gly Asn	
130 135 140	
aat tac caa tta tat cta act gcg ctt gaa gaa tgg gaa gaa aat cca	480
Asn Tyr Gln Leu Tyr Leu Thr Ala Leu Glu Glu Trp Glu Glu Asn Pro	
145 150 155 160	
ttt cga agt cga ggt ttt cga agt cga ggt cca gcc tta cga gat gtg	528
Phe Arg Ser Arg Gly Phe Arg Ser Arg Gly Pro Ala Leu Arg Asp Val	
165 170 175	
cga aat cga ttt gaa atc ctg gat agt tta ttt acg caa tat atg cca	576
Arg Asn Arg Phe Glu Ile Leu Asp Ser Leu Phe Thr Gln Tyr Met Pro	
180 185 190	
tct ttt aga gtg aca aat ttt gaa gta cca ttc ctt act gta tat gca	624
Ser Phe Arg Val Thr Asn Phe Glu Val Pro Phe Leu Thr Val Tyr Ala	
195 200 205	
atg gca gcc aac ctt cat tta ctg tta tta aag gac gcg tca att ttt	672
Met Ala Ala Asn Leu His Leu Leu Leu Leu Lys Asp Ala Ser Ile Phe	
210 215 220	
gga gaa gaa tgg gga tgg tca aca act act att aat aac tat tat gat	720
Gly Glu Glu Trp Gly Trp Ser Thr Thr Thr Ile Asn Asn Tyr Tyr Asp	
225 230 235 240	
cgt caa atg aaa ctt act gca gaa tat tct gat cac tgt gta aag tgg	768
Arg Gln Met Lys Leu Thr Ala Glu Tyr Ser Asp His Cys Val Lys Trp	
245 250 255	
tat gaa act ggt tta gca aaa tta aaa ggc acg agc gct aaa caa tgg	816
Tyr Glu Thr Gly Leu Ala Lys Leu Lys Gly Thr Ser Ala Lys Gln Trp	
260 265 270	
gtt gac tat aac caa ttc cgt aga gaa atg aca ctg gcg gtt tta gat	864
Val Asp Tyr Asn Gln Phe Arg Arg Glu Met Thr Leu Ala Val Leu Asp	
275 280 285	
gtt gtt gca tta ttc cca aat tat gac aca cgc acg tac cca atg gaa	912
Val Val Ala Leu Phe Pro Asn Tyr Asp Thr Arg Thr Tyr Pro Met Glu	
290 295 300	
acg aaa gca caa cta aca agg gaa gta tat aca gat cca ctg ggc gcg	960
Thr Lys Ala Gln Leu Thr Arg Glu Val Tyr Thr Asp Pro Leu Gly Ala	
305 310 315 320	
gta aac gtg tct tca att ggt tcc tgg tat gac aaa gca cct tct ttc	1008
Val Asn Val Ser Ser Ile Gly Ser Trp Tyr Asp Lys Ala Pro Ser Phe	
325 330 335	

gga gtg ata gaa tca tcc gtt att cga cca ccc cat gta ttt gat tat	1056
Gly Val Ile Glu Ser Ser Val Ile Arg Pro Pro His Val Phe Asp Tyr	
340 345 350	
ata acg gga ctc aca gtg tat aca caa tca aga agc att tct tcc gct	1104
Ile Thr Gly Leu Thr Val Tyr Thr Gln Ser Arg Ser Ile Ser Ser Ala	
355 360 365	
cgc tat ata aga cat tgg gct ggt cat caa ata agc tac cat cgt gtc	1152
Arg Tyr Ile Arg His Trp Ala Gly His Gln Ile Ser Tyr His Arg Val	
370 375 380	
agt agg ggt agt aat ctt caa caa atg tat gga act aat caa aat cta	1200
Ser Arg Gly Ser Asn Leu Gln Gln Met Tyr Gly Thr Asn Gln Asn Leu	
385 390 395 400	
cac agc act agt acc ttt gat ttt acg aat tat gat att tac aag act	1248
His Ser Thr Ser Thr Phe Asp Phe Thr Asn Tyr Asp Ile Tyr Lys Thr	
405 410 415	
cta tca aag gat gca gta ctc ctt gat att gtt tac cct ggt tat acg	1296
Leu Ser Lys Asp Ala Val Leu Leu Asp Ile Val Tyr Pro Gly Tyr Thr	
420 425 430	
tat ata ttt ttt gga atg cca gaa gtc gag ttt ttc atg gta aac caa	1344
Tyr Ile Phe Phe Gly Met Pro Glu Val Glu Phe Phe Met Val Asn Gln	
435 440 445	
ttg aat aat acc aga aag acg tta aag tat aat cca gtt tcc aaa gat	1392
Leu Asn Asn Thr Arg Lys Thr Leu Lys Tyr Asn Pro Val Ser Lys Asp	
450 455 460	
att ata gcg agt aca aga gat tcg gaa tta gaa tta cct cca gaa act	1440
Ile Ile Ala Ser Thr Arg Asp Ser Glu Leu Glu Leu Pro Pro Glu Thr	
465 470 475 480	
tca gat caa cca aat tat gag tca tat agc cat aga tta tgt cat atc	1488
Ser Asp Gln Pro Asn Tyr Glu Ser Tyr Ser His Arg Leu Cys His Ile	
485 490 495	
aca agt att ccc gcg acg ggt aac act acc gga tta gta cct gta ttt	1536
Thr Ser Ile Pro Ala Thr Gly Asn Thr Thr Gly Leu Val Pro Val Phe	
500 505 510	
tct tgg aca cat cga agt gca gat tta aac aat aca ata tat tca gat	1584
Ser Trp Thr His Arg Ser Ala Asp Leu Asn Asn Thr Ile Tyr Ser Asp	
515 520 525	
aaa atc act caa att ccg gcc gtt aaa tgt tgg gat aat tta ccg ttt	1632
Lys Ile Thr Gln Ile Pro Ala Val Lys Cys Trp Asp Asn Leu Pro Phe	
530 535 540	
gtt cca gtg gta aaa gga cca gga cat aca gga ggg gat tta tta cag	1680
Val Pro Val Val Lys Gly Pro Gly His Thr Gly Gly Asp Leu Leu Gln	
545 550 555 560	
tat aat aga agt act ggt tct gta gga acc tta ttt cta gct cga tat	1728

Tyr Asn Arg Ser Thr Gly Ser Val Gly Thr Leu Phe Leu Ala Arg Tyr	
565	570 575
ggc cta gca tta gaa aaa gca ggg aaa tat cgt gta aga ctg aga tat	1776
Gly Leu Ala Leu Glu Lys Ala Gly Lys Tyr Arg Val Arg Leu Arg Tyr	
580	585 590
gct act gat gca gat att gta ttg cat gta aac gat gct cag att cag	1824
Ala Thr Asp Ala Asp Ile Val Leu His Val Asn Asp Ala Gln Ile Gln	
595	600 605
atg cca aaa aca atg aac cca ggt gag gat ctg aca tct aaa act ttt	1872
Met Pro Lys Thr Met Asn Pro Gly Glu Asp Leu Thr Ser Lys Thr Phe	
610	615 620
aaa gtt gca gat gct atc aca aca gtt aat tta gca aca gat agt tcg	1920
Lys Val Ala Asp Ala Ile Thr Thr Val Asn Leu Ala Thr Asp Ser Ser	
625	630 635 640
gtt gca gtt aaa cat aat tta ggt gaa gac cct aat tca aca tta tct	1968
Val Ala Val Lys His Asn Leu Gly Glu Asp Pro Asn Ser Thr Leu Ser	
645	650 655
ggc ata gtt tac gtt gac cga atc gaa ttc atc cca gta gat gag aca	2016
Gly Ile Val Tyr Val Asp Arg Ile Glu Phe Ile Pro Val Asp Glu Thr	
660	665 670
tat gaa gcg gaa	2028
Tyr Glu Ala Glu	
675	

<210> 72
 <211> 676
 <212> PRT
 <213> *Bacillus thuringiensis* (mutated)

<400> 72

Met Ser Pro Asn Asn Gln Asn Glu Tyr Glu Ile Ile Asp Ala Thr Pro	
1 5 10 15	
Ser Thr Ser Val Ser Asn Asp Ser Asn Arg Tyr Pro Phe Ala Asn Glu	
20 25 30	
Pro Thr Asn Ala Leu Gln Asn Met Asp Tyr Lys Asp Tyr Leu Lys Met	
35 40 45	
Ser Ala Gly Asn Ala Ser Glu Tyr Pro Gly Ser Pro Glu Val Leu Val	
50 55 60	
Ser Gly Gln Asp Ala Ala Lys Ala Ala Ile Asp Ile Val Gly Lys Leu	
65 70 75 80	
Leu Ser Gly Leu Gly Val Pro Phe Val Gly Pro Ile Val Ser Leu Tyr	
85 90 95	
Thr Gln Leu Ile Asp Ile Leu Trp Pro Ser Gly Glu Lys Ser Gln Trp	
100 105 110	
Glu Ile Phe Met Glu Gln Val Glu Glu Leu Ile Asn Gln Lys Ile Ala	
115 120 125	
Glu Tyr Ala Arg Asn Lys Ala Leu Ser Glu Leu Glu Gly Leu Gly Asn	
130 135 140	
Asn Tyr Gln Leu Tyr Leu Thr Ala Leu Glu Glu Trp Glu Glu Asn Pro	

145					150					155				160
Phe	Arg	Ser	Arg	Gly	Phe	Arg	Ser	Arg	Gly	Pro	Ala	Leu	Arg	Asp
				165					170					175
Arg	Asn	Arg	Phe	Glu	Ile	Leu	Asp	Ser	Leu	Phe	Thr	Gln	Tyr	Met
			180					185					190	
Ser	Phe	Arg	Val	Thr	Asn	Phe	Glu	Val	Pro	Phe	Leu	Thr	Val	Tyr
		195					200					205		
Met	Ala	Ala	Asn	Leu	His	Leu	Leu	Leu	Leu	Lys	Asp	Ala	Ser	Ile
	210					215					220			
Gly	Glu	Glu	Trp	Gly	Trp	Ser	Thr	Thr	Thr	Ile	Asn	Asn	Tyr	Tyr
225					230					235				240
Arg	Gln	Met	Lys	Leu	Thr	Ala	Glu	Tyr	Ser	Asp	His	Cys	Val	Lys
			245						250					255
Tyr	Glu	Thr	Gly	Leu	Ala	Lys	Leu	Lys	Gly	Thr	Ser	Ala	Lys	Gln
			260					265					270	
Val	Asp	Tyr	Asn	Gln	Phe	Arg	Arg	Glu	Met	Thr	Leu	Ala	Val	Leu
	275					280						285		
Val	Val	Ala	Leu	Phe	Pro	Asn	Tyr	Asp	Thr	Arg	Thr	Tyr	Pro	Met
	290					295					300			
Thr	Lys	Ala	Gln	Leu	Thr	Arg	Glu	Val	Tyr	Thr	Asp	Pro	Leu	Gly
305					310					315				320
Val	Asn	Val	Ser	Ser	Ile	Gly	Ser	Trp	Tyr	Asp	Lys	Ala	Pro	Ser
			325						330					335
Gly	Val	Ile	Glu	Ser	Ser	Val	Ile	Arg	Pro	Pro	His	Val	Phe	Asp
			340					345				350		
Ile	Thr	Gly	Leu	Thr	Val	Tyr	Thr	Gln	Ser	Arg	Ser	Ile	Ser	Ser
	355						360				365			
Arg	Tyr	Ile	Arg	His	Trp	Ala	Gly	His	Gln	Ile	Ser	Tyr	His	Arg
	370				375					380				
Ser	Arg	Gly	Ser	Asn	Leu	Gln	Gln	Met	Tyr	Gly	Thr	Asn	Gln	Asn
385				390						395				400
His	Ser	Thr	Ser	Thr	Phe	Asp	Phe	Thr	Asn	Tyr	Asp	Ile	Tyr	Lys
			405						410					415
Leu	Ser	Lys	Asp	Ala	Val	Leu	Leu	Asp	Ile	Val	Tyr	Pro	Gly	Tyr
		420						425				430		
Tyr	Ile	Phe	Phe	Gly	Met	Pro	Glu	Val	Glu	Phe	Phe	Met	Val	Asn
	435						440				445			
Leu	Asn	Asn	Thr	Arg	Lys	Thr	Leu	Lys	Tyr	Asn	Pro	Val	Ser	Lys
	450				455					460				
Ile	Ile	Ala	Ser	Thr	Arg	Asp	Ser	Glu	Leu	Glu	Leu	Pro	Pro	Glu
465					470				475					480
Ser	Asp	Gln	Pro	Asn	Tyr	Glu	Ser	Tyr	Ser	His	Arg	Leu	Cys	His
			485					490					495	
Thr	Ser	Ile	Pro	Ala	Thr	Gly	Asn	Thr	Thr	Gly	Leu	Val	Pro	Val
		500						505				510		
Ser	Trp	Thr	His	Arg	Ser	Ala	Asp	Leu	Asn	Asn	Thr	Ile	Tyr	Ser
	515					520					525			
Lys	Ile	Thr	Gln	Ile	Pro	Ala	Val	Lys	Cys	Trp	Asp	Asn	Leu	Pro
	530					535				540				
Val	Pro	Val	Val	Lys	Gly	Pro	Gly	His	Thr	Gly	Gly	Asp	Leu	Leu
545				550					555					560
Tyr	Asn	Arg	Ser	Thr	Gly	Ser	Val	Gly	Thr	Leu	Phe	Leu	Ala	Arg
			565					570				575		
Gly	Leu	Ala	Leu	Glu	Lys	Ala	Gly	Lys	Tyr	Arg	Val	Arg	Leu	Arg
		580					585					590		
Ala	Thr	Asp	Ala	Asp	Ile	Val	Leu	His	Val	Asn	Asp	Ala	Gln	Ile
		595				600						605		

Met Pro Lys Thr Met Asn Pro Gly Glu Asp Leu Thr Ser Lys Thr Phe
610 615 620
Lys Val Ala Asp Ala Ile Thr Thr Val Asn Leu Ala Thr Asp Ser Ser
625 630 635 640
Val Ala Val Lys His Asn Leu Gly Glu Asp Pro Asn Ser Thr Leu Ser
645 650 655
Gly Ile Val Tyr Val Asp Arg Ile Glu Phe Ile Pro Val Asp Glu Thr
660 665 670
Tyr Glu Ala Glu
675

<210> 73
<211> 2025
<212> DNA
<213> *Bacillus thuringiensis* (mutated)

<220>
<221> CDS
<222> (1)...(2025)

<400> 73
atg agt cca aat aat caa aat gaa tat gaa att ata gat gcg aca cct 48
Met Ser Pro Asn Asn Gln Asn Glu Tyr Glu Ile Ile Asp Ala Thr Pro
1 5 10 15
tct act tct gta tcc aat gat tct aac aga tac cct ttt gcg aat gag 96
Ser Thr Ser Val Ser Asn Asp Ser Asn Arg Tyr Pro Phe Ala Asn Glu
20 25 30
cca aca aat gcg cta caa aat atg gat tat aaa gat tat tta aaa atg 144
Pro Thr Asn Ala Leu Gln Asn Met Asp Tyr Lys Asp Tyr Leu Lys Met
35 40 45
tct gcg gga aat gct agt gaa tac cct ggt tca cct gaa gta ctt gtt 192
Ser Ala Gly Asn Ala Ser Glu Tyr Pro Gly Ser Pro Glu Val Leu Val
50 55 60
agc gga caa gat gca gct aag gcc gca att gat ata gta ggt aaa tta 240
Ser Gly Gln Asp Ala Ala Lys Ala Ala Ile Asp Ile Val Gly Lys Leu
65 70 75 80
cta tca ggt tta ggg gtc cca ttt gtt ggg ccg ata gtg agt ctt tat 288
Leu Ser Gly Leu Gly Val Pro Phe Val Gly Pro Ile Val Ser Leu Tyr
85 90 95
act caa ctt att gat att ctg tgg cct tca ggg gaa aag agt caa tgg 336
Thr Gln Leu Ile Asp Ile Leu Trp Pro Ser Gly Glu Lys Ser Gln Trp
100 105 110
gaa att ttt atg gaa caa gta gaa gaa ctc att aat caa aaa ata gca 384
Glu Ile Phe Met Glu Gln Val Glu Glu Leu Ile Asn Gln Lys Ile Ala
115 120 125
gaa tat gca agg aat aaa gcg ctt tcg gaa tta gaa gga tta ggt aat 432
Glu Tyr Ala Arg Asn Lys Ala Leu Ser Glu Leu Glu Gly Leu Gly Asn
130 135 140

aat tac caa tta tat cta act gcg ctt gaa gaa tgg gaa gaa aat cca	480
Asn Tyr Gln Leu Tyr Leu Thr Ala Leu Glu Glu Trp Glu Glu Asn Pro	
145 150 155 160	
ttt cga agt cga ggt ttt cga agt cga ggt gcc tta cga gat gtg cga	528
Phe Arg Ser Arg Gly Phe Arg Ser Arg Gly Ala Leu Arg Asp Val Arg	
165 170 175	
aat cga ttt gaa atc ctg gat agt tta ttt acg caa tat atg cca tct	576
Asn Arg Phe Glu Ile Leu Asp Ser Leu Phe Thr Gln Tyr Met Pro Ser	
180 185 190	
ttt aga gtg aca aat ttt gaa gta cca ttc ctt act gta tat gca atg	624
Phe Arg Val Thr Asn Phe Glu Val Pro Phe Leu Thr Val Tyr Ala Met	
195 200 205	
gca gcc aac ctt cat tta ctg tta tta aag gac gcg tca att ttt gga	672
Ala Ala Asn Leu His Leu Leu Leu Leu Lys Asp Ala Ser Ile Phe Gly	
210 215 220	
gaa gaa tgg gga tgg tca aca act act att aat aac tat tat gat cgt	720
Glu Glu Trp Gly Trp Ser Thr Thr Thr Ile Asn Asn Tyr Tyr Asp Arg	
225 230 235 240	
caa atg aaa ctt act gca gaa tat tct gat cac tgt gta aag tgg tat	768
Gln Met Lys Leu Thr Ala Glu Tyr Ser Asp His Cys Val Lys Trp Tyr	
245 250 255	
gaa act ggt tta gca aaa tta aaa ggc acg agc gct aaa caa tgg gtt	816
Glu Thr Gly Leu Ala Lys Leu Lys Gly Thr Ser Ala Lys Gln Trp Val	
260 265 270	
gac tat aac caa ttc cgt aga gaa atg aca ctg gcg gtt tta gat gtt	864
Asp Tyr Asn Gln Phe Arg Arg Glu Met Thr Leu Ala Val Leu Asp Val	
275 280 285	
gtt gca tta ttc cca aat tat gac aca cgc acg tac cca atg gaa acg	912
Val Ala Leu Phe Pro Asn Tyr Asp Thr Arg Thr Tyr Pro Met Glu Thr	
290 295 300	
aaa gca caa cta aca agg gaa gta tat aca gat cca ctg ggc gcg gta	960
Lys Ala Gln Leu Thr Arg Glu Val Tyr Thr Asp Pro Leu Gly Ala Val	
305 310 315 320	
aac gtg tct tca att ggt tcc tgg tat gac aaa gca cct tct ttc gga	1008
Asn Val Ser Ser Ile Gly Ser Trp Tyr Asp Lys Ala Pro Ser Phe Gly	
325 330 335	
gtg ata gaa tca tcc gtt att cga cca ccc cat gta ttt gat tat ata	1056
Val Ile Glu Ser Ser Val Ile Arg Pro Pro His Val Phe Asp Tyr Ile	
340 345 350	
acg gga ctc aca gtg tat aca caa tca aga agc att tct tcc gct cgc	1104
Thr Gly Leu Thr Val Tyr Thr Gln Ser Arg Ser Ile Ser Ser Ala Arg	
355 360 365	

tat ata aga cat tgg gct ggt cat caa ata agc tac cat cgt gtc agt	1152
Tyr Ile Arg His Trp Ala Gly His Gln Ile Ser Tyr His Arg Val Ser	
370 375 380	
agg ggt agt aat ctt caa caa atg tat gga act aat caa aat cta cac	1200
Arg Gly Ser Asn Leu Gln Gln Met Tyr Gly Thr Asn Gln Asn Leu His	
385 390 395 400	
agc act agt acc ttt gat ttt acg aat tat gat att tac aag act cta	1248
Ser Thr Ser Thr Phe Asp Phe Thr Asn Tyr Asp Ile Tyr Lys Thr Leu	
405 410 415	
tca aag gat gca gta ctc ctt gat att gtt tac cct ggt tat acg tat	1296
Ser Lys Asp Ala Val Leu Leu Asp Ile Val Tyr Pro Gly Tyr Thr Tyr	
420 425 430	
ata ttt ttt gga atg cca gaa gtc gag ttt ttc atg gta aac caa ttg	1344
Ile Phe Phe Gly Met Pro Glu Val Glu Phe Phe Met Val Asn Gln Leu	
435 440 445	
aat aat acc aga aag acg tta aag tat aat cca gtt tcc aaa gat att	1392
Asn Asn Thr Arg Lys Thr Leu Lys Tyr Asn Pro Val Ser Lys Asp Ile	
450 455 460	
ata gcg agt aca aga gat tcg gaa tta gaa tta cct cca gaa act tca	1440
Ile Ala Ser Thr Arg Asp Ser Glu Leu Glu Leu Pro Pro Glu Thr Ser	
465 470 475 480	
gat caa cca aat tat gag tca tat agc cat aga tta tgt cat atc aca	1488
Asp Gln Pro Asn Tyr Glu Ser Tyr Ser His Arg Leu Cys His Ile Thr	
485 490 495	
agt att ccc gcg acg ggt aac act acc gga tta gta cct gta ttt tct	1536
Ser Ile Pro Ala Thr Gly Asn Thr Thr Gly Leu Val Pro Val Phe Ser	
500 505 510	
tgg aca cat cga agt gca gat tta aac aat aca ata tat tca gat aaa	1584
Trp Thr His Arg Ser Ala Asp Leu Asn Asn Thr Ile Tyr Ser Asp Lys	
515 520 525	
atc act caa att ccg gcc gtt aaa tgt tgg gat aat tta ccg ttt gtt	1632
Ile Thr Gln Ile Pro Ala Val Lys Cys Trp Asp Asn Leu Pro Phe Val	
530 535 540	
cca gtg gta aaa gga cca gga cat aca gga ggg gat tta tta cag tat	1680
Pro Val Val Lys Gly Pro Gly His Thr Gly Gly Asp Leu Leu Gln Tyr	
545 550 555 560	
aat aga agt act ggt tct gta gga acc tta ttt cta gct cga tat ggc	1728
Asn Arg Ser Thr Gly Ser Val Gly Thr Leu Phe Leu Ala Arg Tyr Gly	
565 570 575	
cta gca tta gaa aaa gca ggg aaa tat cgt gta aga ctg aga tat gct	1776
Leu Ala Leu Glu Lys Ala Gly Lys Tyr Arg Val Arg Leu Arg Tyr Ala	
580 585 590	
act gat gca gat att gta ttg cat gta aac gat gct cag att cag atg	1824

Thr	Asp	Ala	Asp	Ile	Val	Leu	His	Val	Asn	Asp	Ala	Gln	Ile	Gln	Met	
		595					600					605				
cca	aaa	aca	atg	aac	cca	ggg	gag	gat	ctg	aca	tct	aaa	act	ttt	aaa	1872
Pro	Lys	Thr	Met	Asn	Pro	Gly	Glu	Asp	Leu	Thr	Ser	Lys	Thr	Phe	Lys	
	610					615					620					
gtt	gca	gat	gct	atc	aca	aca	gtt	aat	tta	gca	aca	gat	agt	tcg	gtt	1920
Val	Ala	Asp	Ala	Ile	Thr	Thr	Val	Asn	Leu	Ala	Thr	Asp	Ser	Ser	Val	
	625				630					635					640	
gca	gtt	aaa	cat	aat	tta	ggg	gaa	gac	cct	aat	tca	aca	tta	tct	ggg	1968
Ala	Val	Lys	His	Asn	Leu	Gly	Glu	Asp	Pro	Asn	Ser	Thr	Leu	Ser	Gly	
				645					650					655		
ata	gtt	tac	gtt	gac	cga	atc	gaa	ttc	atc	cca	gta	gat	gag	aca	tat	2016
Ile	Val	Tyr	Val	Asp	Arg	Ile	Glu	Phe	Ile	Pro	Val	Asp	Glu	Thr	Tyr	
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gaa	gcg	gaa														2025
Glu	Ala	Glu														
		675														

<210> 74

<211> 675

<212> PRT

<213> Bacillus thuringiensis (mutated)

<400> 74

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			20					25					30			
Pro	Thr	Asn	Ala	Leu	Gln	Asn	Met	Asp	Tyr	Lys	Asp	Tyr	Leu	Lys	Met	
		35					40					45				
Ser	Ala	Gly	Asn	Ala	Ser	Glu	Tyr	Pro	Gly	Ser	Pro	Glu	Val	Leu	Val	
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Ser	Gly	Gln	Asp	Ala	Ala	Lys	Ala	Ala	Ile	Asp	Ile	Val	Gly	Lys	Leu	
	65			70					75						80	
Leu	Ser	Gly	Leu	Gly	Val	Pro	Phe	Val	Gly	Pro	Ile	Val	Ser	Leu	Tyr	
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Thr	Gln	Leu	Ile	Asp	Ile	Leu	Trp	Pro	Ser	Gly	Glu	Lys	Ser	Gln	Trp	
		100					105					110				
Glu	Ile	Phe	Met	Glu	Gln	Val	Glu	Glu	Leu	Ile	Asn	Gln	Lys	Ile	Ala	
	115						120					125				
Glu	Tyr	Ala	Arg	Asn	Lys	Ala	Leu	Ser	Glu	Leu	Glu	Gly	Leu	Gly	Asn	
	130				135						140					
Asn	Tyr	Gln	Leu	Tyr	Leu	Thr	Ala	Leu	Glu	Glu	Trp	Glu	Glu	Asn	Pro	
	145			150					155						160	
Phe	Arg	Ser	Arg	Gly	Phe	Arg	Ser	Arg	Gly	Ala	Leu	Arg	Asp	Val	Arg	
			165					170						175		
Asn	Arg	Phe	Glu	Ile	Leu	Asp	Ser	Leu	Phe	Thr	Gln	Tyr	Met	Pro	Ser	
		180					185					190				
Phe	Arg	Val	Thr	Asn	Phe	Glu	Val	Pro	Phe	Leu	Thr	Val	Tyr	Ala	Met	
	195					200						205				
Ala	Ala	Asn	Leu	His	Leu	Leu	Leu	Leu	Lys	Asp	Ala	Ser	Ile	Phe	Gly	

210	215	220
Glu Glu Trp Gly Trp Ser Thr Thr Thr Ile Asn Asn Tyr Tyr Asp Arg		
225	230	235
Gln Met Lys Leu Thr Ala Glu Tyr Ser Asp His Cys Val Lys Trp Tyr		
	245	250
Glu Thr Gly Leu Ala Lys Leu Lys Gly Thr Ser Ala Lys Gln Trp Val		
	260	265
Asp Tyr Asn Gln Phe Arg Arg Glu Met Thr Leu Ala Val Leu Asp Val		
	275	280
Val Ala Leu Phe Pro Asn Tyr Asp Thr Arg Thr Tyr Pro Met Glu Thr		
	290	295
Lys Ala Gln Leu Thr Arg Glu Val Tyr Thr Asp Pro Leu Gly Ala Val		
305	310	315
Asn Val Ser Ser Ile Gly Ser Trp Tyr Asp Lys Ala Pro Ser Phe Gly		
	325	330
Val Ile Glu Ser Ser Val Ile Arg Pro Pro His Val Phe Asp Tyr Ile		
	340	345
Thr Gly Leu Thr Val Tyr Thr Gln Ser Arg Ser Ile Ser Ser Ala Arg		
	355	360
Tyr Ile Arg His Trp Ala Gly His Gln Ile Ser Tyr His Arg Val Ser		
370	375	380
Arg Gly Ser Asn Leu Gln Gln Met Tyr Gly Thr Asn Gln Asn Leu His		
385	390	395
Ser Thr Ser Thr Phe Asp Phe Thr Asn Tyr Asp Ile Tyr Lys Thr Leu		
	405	410
Ser Lys Asp Ala Val Leu Leu Asp Ile Val Tyr Pro Gly Tyr Thr Tyr		
	420	425
Ile Phe Phe Gly Met Pro Glu Val Glu Phe Phe Met Val Asn Gln Leu		
	435	440
Asn Asn Thr Arg Lys Thr Leu Lys Tyr Asn Pro Val Ser Lys Asp Ile		
	450	455
Ile Ala Ser Thr Arg Asp Ser Glu Leu Glu Leu Pro Pro Glu Thr Ser		
465	470	475
Asp Gln Pro Asn Tyr Glu Ser Tyr Ser His Arg Leu Cys His Ile Thr		
	485	490
Ser Ile Pro Ala Thr Gly Asn Thr Thr Gly Leu Val Pro Val Phe Ser		
	500	505
Trp Thr His Arg Ser Ala Asp Leu Asn Asn Thr Ile Tyr Ser Asp Lys		
	515	520
Ile Thr Gln Ile Pro Ala Val Lys Cys Trp Asp Asn Leu Pro Phe Val		
	530	535
Pro Val Val Lys Gly Pro Gly His Thr Gly Gly Asp Leu Leu Gln Tyr		
545	550	555
Asn Arg Ser Thr Gly Ser Val Gly Thr Leu Phe Leu Ala Arg Tyr Gly		
	565	570
Leu Ala Leu Glu Lys Ala Gly Lys Tyr Arg Val Arg Leu Arg Tyr Ala		
	580	585
Thr Asp Ala Asp Ile Val Leu His Val Asn Asp Ala Gln Ile Gln Met		
	595	600
Pro Lys Thr Met Asn Pro Gly Glu Asp Leu Thr Ser Lys Thr Phe Lys		
	610	615
Val Ala Asp Ala Ile Thr Thr Val Asn Leu Ala Thr Asp Ser Ser Val		
625	630	635
Ala Val Lys His Asn Leu Gly Glu Asp Pro Asn Ser Thr Leu Ser Gly		
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Glu Ala Glu
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<210> 75
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<212> DNA
<213> *Bacillus thuringiensis* (mutated)

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<221> CDS
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tct act tct gta tcc aat gat tct aac aga tac cct ttt gcg aat gag 96
Ser Thr Ser Val Ser Asn Asp Ser Asn Arg Tyr Pro Phe Ala Asn Glu
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cca aca aat gcg cta caa aat atg gat tat aaa gat tat tta aaa atg 144
Pro Thr Asn Ala Leu Gln Asn Met Asp Tyr Lys Asp Tyr Leu Lys Met
35 40 45

tct gcg gga aat gct agt gaa tac cct ggt tca cct gaa gta ctt gtt 192
Ser Ala Gly Asn Ala Ser Glu Tyr Pro Gly Ser Pro Glu Val Leu Val
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agc gga caa gat gca gct aag gcc gca att gat ata gta ggt aaa tta 240
Ser Gly Gln Asp Ala Ala Lys Ala Ala Ile Asp Ile Val Gly Lys Leu
65 70 75 80

cta tca ggt tta ggg gtc cca ttt gtt ggg ccg ata gtg agt ctt tat 288
Leu Ser Gly Leu Gly Val Pro Phe Val Gly Pro Ile Val Ser Leu Tyr
85 90 95

act caa ctt att gat att ctg tgg cct tca ggg gaa aag agt caa tgg 336
Thr Gln Leu Ile Asp Ile Leu Trp Pro Ser Gly Glu Lys Ser Gln Trp
100 105 110

gaa att ttt atg gaa caa gta gaa gaa ctc att aat caa aaa ata gca 384
Glu Ile Phe Met Glu Gln Val Glu Glu Leu Ile Asn Gln Lys Ile Ala
115 120 125

gaa tat gca agg aat aaa gcg ctt tcg gaa tta gaa gga tta ggt aat 432
Glu Tyr Ala Arg Asn Lys Ala Leu Ser Glu Leu Glu Gly Leu Gly Asn
130 135 140

aat tac caa tta tat cta act gcg ctt gaa gaa tgg gaa gaa aat cca 480
Asn Tyr Gln Leu Tyr Leu Thr Ala Leu Glu Glu Trp Glu Glu Asn Pro
145 150 155 160

aat ggt tcc cgg ttt cga agt cga ggt gcc tta cga gat gtg cga aat 528
Asn Gly Ser Arg Phe Arg Ser Arg Gly Ala Leu Arg Asp Val Arg Asn
165 170 175

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cga ttt gaa atc ctg gat agt tta ttt acg caa tat atg cca tct ttt	576
Arg Phe Glu Ile Leu Asp Ser Leu Phe Thr Gln Tyr Met Pro Ser Phe	
180 185 190	
aga gtg aca aat ttt gaa gta cca ttc ctt act gta tat gca atg gca	624
Arg Val Thr Asn Phe Glu Val Pro Phe Leu Thr Val Tyr Ala Met Ala	
195 200 205	
gcc aac ctt cat tta ctg tta tta aag gac gcg tca att ttt gga gaa	672
Ala Asn Leu His Leu Leu Leu Leu Lys Asp Ala Ser Ile Phe Gly Glu	
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gaa tgg gga tgg tca aca act act att aat aac tat tat gat cgt caa	720
Glu Trp Gly Trp Ser Thr Thr Thr Ile Asn Asn Tyr Tyr Asp Arg Gln	
225 230 235 240	
atg aaa ctt act gca gaa tat tct gat cac tgt gta aag tgg tat gaa	768
Met Lys Leu Thr Ala Glu Tyr Ser Asp His Cys Val Lys Trp Tyr Glu	
245 250 255	
act ggt tta gca aaa tta aaa ggc acg agc gct aaa caa tgg gtt gac	816
Thr Gly Leu Ala Lys Leu Lys Gly Thr Ser Ala Lys Gln Trp Val Asp	
260 265 270	
tat aac caa ttc cgt aga gaa atg aca ctg gcg gtt tta gat gtt gtt	864
Tyr Asn Gln Phe Arg Arg Glu Met Thr Leu Ala Val Leu Asp Val Val	
275 280 285	
gca tta ttc cca aat tat gac aca cgc acg tac cca atg gaa acg aaa	912
Ala Leu Phe Pro Asn Tyr Asp Thr Arg Thr Tyr Pro Met Glu Thr Lys	
290 295 300	
gca caa cta aca agg gaa gta tat aca gat cca ctg ggc gcg gta aac	960
Ala Gln Leu Thr Arg Glu Val Tyr Thr Asp Pro Leu Gly Ala Val Asn	
305 310 315 320	
gtg tct tca att ggt tcc tgg tat gac aaa gca cct tct ttc gga gtg	1008
Val Ser Ser Ile Gly Ser Trp Tyr Asp Lys Ala Pro Ser Phe Gly Val	
325 330 335	
ata gaa tca tcc gtt att cga cca ccc cat gta ttt gat tat ata acg	1056
Ile Glu Ser Ser Val Ile Arg Pro Pro His Val Phe Asp Tyr Ile Thr	
340 345 350	
gga ctc aca gtg tat aca caa tca aga agc att tct tcc gct cgc tat	1104
Gly Leu Thr Val Tyr Thr Gln Ser Arg Ser Ile Ser Ser Ala Arg Tyr	
355 360 365	
ata aga cat tgg gct ggt cat caa ata agc tac cat cgt gtc agt agg	1152
Ile Arg His Trp Ala Gly His Gln Ile Ser Tyr His Arg Val Ser Arg	
370 375 380	
ggt agt aat ctt caa caa atg tat gga act aat caa aat cta cac agc	1200
Gly Ser Asn Leu Gln Gln Met Tyr Gly Thr Asn Gln Asn Leu His Ser	
385 390 395 400	

act agt acc ttt gat ttt acg aat tat gat att tac aag act cta tca	1248
Thr Ser Thr Phe Asp Phe Thr Asn Tyr Asp Ile Tyr Lys Thr Leu Ser	
405 410 415	
aag gat gca gta ctc ctt gat att gtt tac cct ggt tat acg tat ata	1296
Lys Asp Ala Val Leu Leu Asp Ile Val Tyr Pro Gly Tyr Thr Tyr Ile	
420 425 430	
ttt ttt gga atg cca gaa gtc gag ttt ttc atg gta aac caa ttg aat	1344
Phe Phe Gly Met Pro Glu Val Glu Phe Phe Met Val Asn Gln Leu Asn	
435 440 445	
aat acc aga aag acg tta aag tat aat cca gtt tcc aaa gat att ata	1392
Asn Thr Arg Lys Thr Leu Lys Tyr Asn Pro Val Ser Lys Asp Ile Ile	
450 455 460	
gcg agt aca aga gat tcg gaa tta gaa tta cct cca gaa act tca gat	1440
Ala Ser Thr Arg Asp Ser Glu Leu Glu Leu Pro Pro Glu Thr Ser Asp	
465 470 475 480	
caa cca aat tat gag tca tat agc cat aga tta tgt cat atc aca agt	1488
Gln Pro Asn Tyr Glu Ser Tyr Ser His Arg Leu Cys His Ile Thr Ser	
485 490 495	
att ccc gcg acg ggt aac act acc gga tta gta cct gta ttt tct tgg	1536
Ile Pro Ala Thr Gly Asn Thr Thr Gly Leu Val Pro Val Phe Ser Trp	
500 505 510	
aca cat cga agt gca gat tta aac aat aca ata tat tca gat aaa atc	1584
Thr His Arg Ser Ala Asp Leu Asn Asn Thr Ile Tyr Ser Asp Lys Ile	
515 520 525	
act caa att ccg gcc gtt aaa tgt tgg gat aat tta ccg ttt gtt cca	1632
Thr Gln Ile Pro Ala Val Lys Cys Trp Asp Asn Leu Pro Phe Val Pro	
530 535 540	
gtg gta aaa gga cca gga cat aca gga ggg gat tta tta cag tat aat	1680
Val Val Lys Gly Pro Gly His Thr Gly Gly Asp Leu Leu Gln Tyr Asn	
545 550 555 560	
aga agt act ggt tct gta gga acc tta ttt cta gct cga tat ggc cta	1728
Arg Ser Thr Gly Ser Val Gly Thr Leu Phe Leu Ala Arg Tyr Gly Leu	
565 570 575	
gca tta gaa aaa gca ggg aaa tat cgt gta aga ctg aga tat gct act	1776
Ala Leu Glu Lys Ala Gly Lys Tyr Arg Val Arg Leu Arg Tyr Ala Thr	
580 585 590	
gat gca gat att gta ttg cat gta aac gat gct cag att cag atg cca	1824
Asp Ala Asp Ile Val Leu His Val Asn Asp Ala Gln Ile Gln Met Pro	
595 600 605	
aaa aca atg aac cca ggt gag gat ctg aca tct aaa act ttt aaa gtt	1872
Lys Thr Met Asn Pro Gly Glu Asp Leu Thr Ser Lys Thr Phe Lys Val	
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<221> CDS

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tct act tct gta tcc aat gat tct aac aga tac cct ttt gcg aat gag	96
Ser Thr Ser Val Ser Asn Asp Ser Asn Arg Tyr Pro Phe Ala Asn Glu	
20 25 30	
cca aca aat gcg cta caa aat atg gat tat aaa gat tat tta aaa atg	144
Pro Thr Asn Ala Leu Gln Asn Met Asp Tyr Lys Asp Tyr Leu Lys Met	
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tct gcg gga aat gct agt gaa tac cct ggt tca cct gaa gta ctt gtt	192
Ser Ala Gly Asn Ala Ser Glu Tyr Pro Gly Ser Pro Glu Val Leu Val	
50 55 60	
agc gga caa gat gca gct aag gcc gca att gat ata gta ggt aaa tta	240
Ser Gly Gln Asp Ala Ala Lys Ala Ala Ile Asp Ile Val Gly Lys Leu	
65 70 75 80	
cta tca ggt tta ggg gtc cca ttt gtt ggg ccg ata gtg agt ctt tat	288
Leu Ser Gly Leu Gly Val Pro Phe Val Gly Pro Ile Val Ser Leu Tyr	
85 90 95	
act caa ctt att gat att ctg tgg cct tca ggg gaa aag agt caa tgg	336
Thr Gln Leu Ile Asp Ile Leu Trp Pro Ser Gly Glu Lys Ser Gln Trp	
100 105 110	
gaa att ttt atg gaa caa gta gaa gaa ctc att aat caa aaa ata gca	384
Glu Ile Phe Met Glu Gln Val Glu Glu Leu Ile Asn Gln Lys Ile Ala	
115 120 125	
gaa tat gca agg aat aaa gcg ctt tcg gaa tta gaa gga tta ggt aat	432
Glu Tyr Ala Arg Asn Lys Ala Leu Ser Glu Leu Glu Gly Leu Gly Asn	
130 135 140	
aat tac caa tta tat cta act gcg ctt gaa gaa tgg gaa gaa aat cca	480
Asn Tyr Gln Leu Tyr Leu Thr Ala Leu Glu Glu Trp Glu Glu Asn Pro	
145 150 155 160	
aat ggt tcc cgg ttt cga agt cga ggt cca gcc tta cga gat gtg cga	528
Asn Gly Ser Arg Phe Arg Ser Arg Gly Pro Ala Leu Arg Asp Val Arg	
165 170 175	
aat cga ttt gaa atc ctg gat agt tta ttt acg caa tat atg cca tct	576
Asn Arg Phe Glu Ile Leu Asp Ser Leu Phe Thr Gln Tyr Met Pro Ser	
180 185 190	
ttt aga gtg aca aat ttt gaa gta cca ttc ctt act gta tat gca atg	624
Phe Arg Val Thr Asn Phe Glu Val Pro Phe Leu Thr Val Tyr Ala Met	
195 200 205	

gca gcc aac ctt cat tta ctg tta tta aag gac gcg tca att ttt gga	762
Ala Ala Asn Leu His Leu Leu Leu Lys Asp Ala Ser Ile Phe Gly	
210 215 220	
gaa gaa tgg gga tgg tca aca act act att aat aac tat tat gat cgt	720
Glu Glu Trp Gly Trp Ser Thr Thr Thr Ile Asn Asn Tyr Tyr Asp Arg	
225 230 235 240	
caa atg aaa ctt act gca gaa tat tct gat cac tgt gta aag tgg tat	768
Gln Met Lys Leu Thr Ala Glu Tyr Ser Asp His Cys Val Lys Trp Tyr	
245 250 255	
gaa act ggt tta gca aaa tta aaa ggc acg agc gct aaa caa tgg gtt	816
Glu Thr Gly Leu Ala Lys Leu Lys Gly Thr Ser Ala Lys Gln Trp Val	
260 265 270	
gac tat aac caa ttc cgt aga gaa atg aca ctg gcg gtt tta gat gtt	864
Asp Tyr Asn Gln Phe Arg Arg Glu Met Thr Leu Ala Val Leu Asp Val	
275 280 285	
gtt gca tta ttc cca aat tat gac aca cgc acg tac cca atg gaa acg	912
Val Ala Leu Phe Pro Asn Tyr Asp Thr Arg Thr Tyr Pro Met Glu Thr	
290 295 300	
aaa gca caa cta aca agg gaa gta tat aca gat cca ctg ggc gcg gta	960
Lys Ala Gln Leu Thr Arg Glu Val Tyr Thr Asp Pro Leu Gly Ala Val	
305 310 315 320	
aac gtg tct tca att ggt tcc tgg tat gac aaa gca cct tct ttc gga	1008
Asn Val Ser Ser Ile Gly Ser Trp Tyr Asp Lys Ala Pro Ser Phe Gly	
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gtg ata gaa tca tcc gtt att cga cca ccc cat gta ttt gat tat ata	1056
Val Ile Glu Ser Ser Val Ile Arg Pro Pro His Val Phe Asp Tyr Ile	
340 345 350	
acg gga ctc aca gtg tat aca caa tca aga agc att tct tcc gct cgc	1104
Thr Gly Leu Thr Val Tyr Thr Gln Ser Arg Ser Ile Ser Ser Ala Arg	
355 360 365	
tat ata aga cat tgg gct ggt cat caa ata agc tac cat cgt gtc agt	1152
Tyr Ile Arg His Trp Ala Gly His Gln Ile Ser Tyr His Arg Val Ser	
370 375 380	
agg ggt agt aat ctt caa caa atg tat gga act aat caa aat cta cac	1200
Arg Gly Ser Asn Leu Gln Gln Met Tyr Gly Thr Asn Gln Asn Leu His	
385 390 395 400	
agc act agt acc ttt gat ttt acg aat tat gat att tac aag act cta	1248
Ser Thr Ser Thr Phe Asp Phe Thr Asn Tyr Asp Ile Tyr Lys Thr Leu	
405 410 415	
tca aag gat gca gta ctc ctt gat att gtt tac cct ggt tat acg tat	1296
Ser Lys Asp Ala Val Leu Leu Asp Ile Val Tyr Pro Gly Tyr Thr Tyr	
420 425 430	

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Ile Phe Phe Gly Met Pro Glu Val Glu Phe Phe Met Val Asn Gln Leu	
435 440 445	
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Asn Asn Thr Arg Lys Thr Leu Lys Tyr Asn Pro Val Ser Lys Asp Ile	
450 455 460	
ata gcg agt aca aga gat tcg gaa tta gaa tta cct cca gaa act tca	1440
Ile Ala Ser Thr Arg Asp Ser Glu Leu Glu Leu Pro Pro Glu Thr Ser	
465 470 475 480	
gat caa cca aat tat gag tca tat agc cat aga tta tgt cat atc aca	1488
Asp Gln Pro Asn Tyr Glu Ser Tyr Ser His Arg Leu Cys His Ile Thr	
485 490 495	
agt att ccc gcg acg ggt aac act acc gga tta gta cct gta ttt tct	1536
Ser Ile Pro Ala Thr Gly Asn Thr Thr Gly Leu Val Pro Val Phe Ser	
500 505 510	
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Trp Thr His Arg Ser Ala Asp Leu Asn Asn Thr Ile Tyr Ser Asp Lys	
515 520 525	
atc act caa att ccg gcc gtt aaa tgt tgg gat aat tta ccg ttt gtt	1632
Ile Thr Gln Ile Pro Ala Val Lys Cys Trp Asp Asn Leu Pro Phe Val	
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cca gtg gta aaa gga cca gga cat aca gga ggg gat tta tta cag tat	1680
Pro Val Val Lys Gly Pro Gly His Thr Gly Gly Asp Leu Leu Gln Tyr	
545 550 555 560	
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Asn Arg Ser Thr Gly Ser Val Gly Thr Leu Phe Leu Ala Arg Tyr Gly	
565 570 575	
cta gca tta gaa aaa gca ggg aaa tat cgt gta aga ctg aga tat gct	1776
Leu Ala Leu Glu Lys Ala Gly Lys Tyr Arg Val Arg Leu Arg Tyr Ala	
580 585 590	
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Thr Asp Ala Asp Ile Val Leu His Val Asn Asp Ala Gln Ile Gln Met	
595 600 605	
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Pro Lys Thr Met Asn Pro Gly Glu Asp Leu Thr Ser Lys Thr Phe Lys	
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gca gtt aaa cat aat tta ggt gaa gac cct aat tca aca tta tct ggt	1968
Ala Val Lys His Asn Leu Gly Glu Asp Pro Asn Ser Thr Leu Ser Gly	
645 650 655	
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Ile Val Tyr Val Asp Arg Ile Glu Phe Ile Pro Val Asp Glu Thr Tyr
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gaa gcg gaa
Glu Ala

2025

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35 40 45
Ser Ala Gly Asn Ala Ser Glu Tyr Pro Gly Ser Pro Glu Val Leu Val
50 55 60
Ser Gly Gln Asp Ala Ala Lys Ala Ala Ile Asp Ile Val Gly Lys Leu
65 70 75 80
Leu Ser Gly Leu Gly Val Pro Phe Val Gly Pro Ile Val Ser Leu Tyr
85 90 95
Thr Gln Leu Ile Asp Ile Leu Trp Pro Ser Gly Glu Lys Ser Gln Trp
100 105 110
Glu Ile Phe Met Glu Gln Val Glu Glu Leu Ile Asn Gln Lys Ile Ala
115 120 125
Glu Tyr Ala Arg Asn Lys Ala Leu Ser Glu Leu Glu Gly Leu Gly Asn
130 135 140
Asn Tyr Gln Leu Tyr Leu Thr Ala Leu Glu Glu Trp Glu Glu Asn Pro
145 150 155 160
Asn Gly Ser Arg Phe Arg Ser Arg Gly Pro Ala Leu Arg Asp Val Arg
165 170 175
Asn Arg Phe Glu Ile Leu Asp Ser Leu Phe Thr Gln Tyr Met Pro Ser
180 185 190
Phe Arg Val Thr Asn Phe Glu Val Pro Phe Leu Thr Val Tyr Ala Met
195 200 205
Ala Ala Asn Leu His Leu Leu Leu Leu Lys Asp Ala Ser Ile Phe Gly
210 215 220
Glu Glu Trp Gly Trp Ser Thr Thr Thr Ile Asn Asn Tyr Tyr Asp Arg
225 230 235 240
Gln Met Lys Leu Thr Ala Glu Tyr Ser Asp His Cys Val Lys Trp Tyr
245 250 255
Glu Thr Gly Leu Ala Lys Leu Lys Gly Thr Ser Ala Lys Gln Trp Val
260 265 270
Asp Tyr Asn Gln Phe Arg Arg Glu Met Thr Leu Ala Val Leu Asp Val
275 280 285
Val Ala Leu Phe Pro Asn Tyr Asp Thr Arg Thr Tyr Pro Met Glu Thr
290 295 300
Lys Ala Gln Leu Thr Arg Glu Val Tyr Thr Asp Pro Leu Gly Ala Val
305 310 315 320
Asn Val Ser Ser Ile Gly Ser Trp Tyr Asp Lys Ala Pro Ser Phe Gly
325 330 335
Val Ile Glu Ser Ser Val Ile Arg Pro Pro His Val Phe Asp Tyr Ile

1	5	10	15	
tct act tct gta tcc aat gat tct aac aga tac cct ttt gcg aat gag	96			
Ser Thr Ser Val Ser Asn Asp Ser Asn Arg Tyr Pro Phe Ala Asn Glu				
20 25 30				
cca aca aat gcg cta caa aat atg gat tat aaa gat tat tta aaa atg	144			
Pro Thr Asn Ala Leu Gln Asn Met Asp Tyr Lys Asp Tyr Leu Lys Met				
35 40 45				
tct gcg gga aat gct agt gaa tac cct ggt tca cct gaa gta ctt gtt	192			
Ser Ala Gly Asn Ala Ser Glu Tyr Pro Gly Ser Pro Glu Val Leu Val				
50 55 60				
agc gga caa gat gca gct aag gcc gca att gat ata gta ggt aaa tta	240			
Ser Gly Gln Asp Ala Ala Lys Ala Ala Ile Asp Ile Val Gly Lys Leu				
65 70 75 80				
cta tca ggt tta ggg gtc cca ttt gtt ggg ccg ata gtg agt ctt tat	288			
Leu Ser Gly Leu Gly Val Pro Phe Val Gly Pro Ile Val Ser Leu Tyr				
85 90 95				
act caa ctt att gat att ctg tgg cct tca ggg gaa aag agt caa tgg	336			
Thr Gln Leu Ile Asp Ile Leu Trp Pro Ser Gly Glu Lys Ser Gln Trp				
100 105 110				
gaa att ttt atg gaa caa gta gaa gaa ctc att aat caa aaa ata gca	384			
Glu Ile Phe Met Glu Gln Val Glu Glu Leu Ile Asn Gln Lys Ile Ala				
115 120 125				
gaa tat gca agg aat aaa gcg ctt tcg gaa tta gaa gga tta ggt aat	432			
Glu Tyr Ala Arg Asn Lys Ala Leu Ser Glu Leu Glu Gly Leu Gly Asn				
130 135 140				
aat tac caa tta tat cta act gcg ctt gaa gaa tgg gaa gaa aat cca	480			
Asn Tyr Gln Leu Tyr Leu Thr Ala Leu Glu Glu Trp Glu Glu Asn Pro				
145 150 155 160				
ttt cga agt cga ggt cca aat ggt tcc cgg gcc tta cga gat gtg cga	528			
Phe Arg Ser Arg Gly Pro Asn Gly Ser Arg Ala Leu Arg Asp Val Arg				
165 170 175				
aat cga ttt gaa atc ctg gat agt tta ttt acg caa tat atg cca tct	576			
Asn Arg Phe Glu Ile Leu Asp Ser Leu Phe Thr Gln Tyr Met Pro Ser				
180 185 190				
ttt aga gtg aca aat ttt gaa gta cca ttc ctt act gta tat gca atg	624			
Phe Arg Val Thr Asn Phe Glu Val Pro Phe Leu Thr Val Tyr Ala Met				
195 200 205				
gca gcc aac ctt cat tta ctg tta tta aag gac gcg tca att ttt gga	672			
Ala Ala Asn Leu His Leu Leu Leu Leu Lys Asp Ala Ser Ile Phe Gly				
210 215 220				
gaa gaa tgg gga tgg tca aca act act att aat aac tat tat gat cgt	720			
Glu Glu Trp Gly Trp Ser Thr Thr Thr Ile Asn Asn Tyr Tyr Asp Arg				
225 230 235 240				

caa atg aaa ctt act gca gaa tat tct gat cac tgt gta aag tgg tat	768
Gln Met Lys Leu Thr Ala Glu Tyr Ser Asp His Cys Val Lys Trp Tyr	
245 250 255	
gaa act ggt tta gca aaa tta aaa ggc acg agc gct aaa caa tgg gtt	816
Glu Thr Gly Leu Ala Lys Leu Lys Gly Thr Ser Ala Lys Gln Trp Val	
260 265 270	
gac tat aac caa ttc cgt aga gaa atg aca ctg gcg gtt tta gat gtt	864
Asp Tyr Asn Gln Phe Arg Arg Glu Met Thr Leu Ala Val Leu Asp Val	
275 280 285	
gtt gca tta ttc cca aat tat gac aca cgc acg tac cca atg gaa acg	912
Val Ala Leu Phe Pro Asn Tyr Asp Thr Arg Thr Tyr Pro Met Glu Thr	
290 295 300	
aaa gca caa cta aca agg gaa gta tat aca gat cca ctg ggc gcg gta	960
Lys Ala Gln Leu Thr Arg Glu Val Tyr Thr Asp Pro Leu Gly Ala Val	
305 310 315 320	
aac gtg tct tca att ggt tcc tgg tat gac aaa gca cct tct ttc gga	1008
Asn Val Ser Ser Ile Gly Ser Trp Tyr Asp Lys Ala Pro Ser Phe Gly	
325 330 335	
gtg ata gaa tca tcc gtt att cga cca ccc cat gta ttt gat tat ata	1056
Val Ile Glu Ser Ser Val Ile Arg Pro Pro His Val Phe Asp Tyr Ile	
340 345 350	
acg gga ctc aca gtg tat aca caa tca aga agc att tct tcc gct cgc	1104
Thr Gly Leu Thr Val Tyr Thr Gln Ser Arg Ser Ile Ser Ser Ala Arg	
355 360 365	
tat ata aga cat tgg gct ggt cat caa ata agc tac cat cgt gtc agt	1152
Tyr Ile Arg His Trp Ala Gly His Gln Ile Ser Tyr His Arg Val Ser	
370 375 380	
agg ggt agt aat ctt caa caa atg tat gga act aat caa aat cta cac	1200
Arg Gly Ser Asn Leu Gln Gln Met Tyr Gly Thr Asn Gln Asn Leu His	
385 390 395 400	
agc act agt acc ttt gat ttt acg aat tat gat att tac aag act cta	1248
Ser Thr Ser Thr Phe Asp Phe Thr Asn Tyr Asp Ile Tyr Lys Thr Leu	
405 410 415	
tca aag gat gca gta ctc ctt gat att gtt tac cct ggt tat acg tat	1296
Ser Lys Asp Ala Val Leu Leu Asp Ile Val Tyr Pro Gly Tyr Thr Tyr	
420 425 430	
ata ttt ttt gga atg cca gaa gtc gag ttt ttc atg gta aac caa ttg	1344
Ile Phe Phe Gly Met Pro Glu Val Glu Phe Phe Met Val Asn Gln Leu	
435 440 445	
aat aat acc aga aag acg tta aag tat aat cca gtt tcc aaa gat att	1392
Asn Asn Thr Arg Lys Thr Leu Lys Tyr Asn Pro Val Ser Lys Asp Ile	
450 455 460	

ata gcg agt aca aga gat tcg gaa tta gaa tta cct cca gaa act tca	1440
Ile Ala Ser Thr Arg Asp Ser Glu Leu Glu Leu Pro Pro Glu Thr Ser	
465 470 475 480	
gat caa cca aat tat gag tca tat agc cat aga tta tgt cat atc aca	1488
Asp Gln Pro Asn Tyr Glu Ser Tyr Ser His Arg Leu Cys His Ile Thr	
485 490 495	
agt att ccc gcg acg ggt aac act acc gga tta gta cct gta ttt tct	1536
Ser Ile Pro Ala Thr Gly Asn Thr Thr Gly Leu Val Pro Val Phe Ser	
500 505 510	
tgg aca cat cga agt gca gat tta aac aat aca ata tat tca gat aaa	1584
Trp Thr His Arg Ser Ala Asp Leu Asn Asn Thr Ile Tyr Ser Asp Lys	
515 520 525	
atc act caa att ccg gcc gtt aaa tgt tgg gat aat tta ccg ttt gtt	1632
Ile Thr Gln Ile Pro Ala Val Lys Cys Trp Asp Asn Leu Pro Phe Val	
530 535 540	
cca gtg gta aaa gga cca gga cat aca gga ggg gat tta tta cag tat	1680
Pro Val Val Lys Gly Pro Gly His Thr Gly Gly Asp Leu Leu Gln Tyr	
545 550 555 560	
aat aga agt act ggt tct gta gga acc tta ttt cta gct cga tat ggc	1728
Asn Arg Ser Thr Gly Ser Val Gly Thr Leu Phe Leu Ala Arg Tyr Gly	
565 570 575	
cta gca tta gaa aaa gca ggg aaa tat cgt gta aga ctg aga tat gct	1776
Leu Ala Leu Glu Lys Ala Gly Lys Tyr Arg Val Arg Leu Arg Tyr Ala	
580 585 590	
act gat gca gat att gta ttg cat gta aac gat gct cag att cag atg	1824
Thr Asp Ala Asp Ile Val Leu His Val Asn Asp Ala Gln Ile Gln Met	
595 600 605	
cca aaa aca atg aac cca ggt gag gat ctg aca tct aaa act ttt aaa	1872
Pro Lys Thr Met Asn Pro Gly Glu Asp Leu Thr Ser Lys Thr Phe Lys	
610 615 620	
gtt gca gat gct atc aca aca gtt aat tta gca aca gat agt tcg gtt	1920
Val Ala Asp Ala Ile Thr Thr Val Asn Leu Ala Thr Asp Ser Ser Val	
625 630 635 640	
gca gtt aaa cat aat tta ggt gaa gac cct aat tca aca tta tct ggt	1968
Ala Val Lys His Asn Leu Gly Glu Asp Pro Asn Ser Thr Leu Ser Gly	
645 650 655	
ata gtt tac gtt gac cga atc gaa ttc atc cca gta gat gag aca tat	2016
Ile Val Tyr Val Asp Arg Ile Glu Phe Ile Pro Val Asp Glu Thr Tyr	
660 665 670	
gaa gcg gaa	2025
Glu Ala Glu	
675	

<210> 80
 <211> 675
 <212> PRT
 <213> *Bacillus thuringiensis* (mutated)

<400> 80
 Met Ser Pro Asn Asn Gln Asn Glu Tyr Glu Ile Ile Asp Ala Thr Pro
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 20 25 30
 Pro Thr Asn Ala Leu Gln Asn Met Asp Tyr Lys Asp Tyr Leu Lys Met
 35 40 45
 Ser Ala Gly Asn Ala Ser Glu Tyr Pro Gly Ser Pro Glu Val Leu Val
 50 55 60
 Ser Gly Gln Asp Ala Ala Lys Ala Ala Ile Asp Ile Val Gly Lys Leu
 65 70 75 80
 Leu Ser Gly Leu Gly Val Pro Phe Val Gly Pro Ile Val Ser Leu Tyr
 85 90 95
 Thr Gln Leu Ile Asp Ile Leu Trp Pro Ser Gly Glu Lys Ser Gln Trp
 100 105 110
 Glu Ile Phe Met Glu Gln Val Glu Glu Leu Ile Asn Gln Lys Ile Ala
 115 120 125
 Glu Tyr Ala Arg Asn Lys Ala Leu Ser Glu Leu Glu Gly Leu Gly Asn
 130 135 140
 Asn Tyr Gln Leu Tyr Leu Thr Ala Leu Glu Glu Trp Glu Glu Asn Pro
 145 150 155 160
 Phe Arg Ser Arg Gly Pro Asn Gly Ser Arg Ala Leu Arg Asp Val Arg
 165 170 175
 Asn Arg Phe Glu Ile Leu Asp Ser Leu Phe Thr Gln Tyr Met Pro Ser
 180 185 190
 Phe Arg Val Thr Asn Phe Glu Val Pro Phe Leu Thr Val Tyr Ala Met
 195 200 205
 Ala Ala Asn Leu His Leu Leu Leu Lys Asp Ala Ser Ile Phe Gly
 210 215 220
 Glu Glu Trp Gly Trp Ser Thr Thr Thr Ile Asn Asn Tyr Tyr Asp Arg
 225 230 235 240
 Gln Met Lys Leu Thr Ala Glu Tyr Ser Asp His Cys Val Lys Trp Tyr
 245 250 255
 Glu Thr Gly Leu Ala Lys Leu Lys Gly Thr Ser Ala Lys Gln Trp Val
 260 265 270
 Asp Tyr Asn Gln Phe Arg Arg Glu Met Thr Leu Ala Val Leu Asp Val
 275 280 285
 Val Ala Leu Phe Pro Asn Tyr Asp Thr Arg Thr Tyr Pro Met Glu Thr
 290 295 300
 Lys Ala Gln Leu Thr Arg Glu Val Tyr Thr Asp Pro Leu Gly Ala Val
 305 310 315 320
 Asn Val Ser Ser Ile Gly Ser Trp Tyr Asp Lys Ala Pro Ser Phe Gly
 325 330 335
 Val Ile Glu Ser Ser Val Ile Arg Pro Pro His Val Phe Asp Tyr Ile
 340 345 350
 Thr Gly Leu Thr Val Tyr Thr Gln Ser Arg Ser Ile Ser Ser Ala Arg
 355 360 365
 Tyr Ile Arg His Trp Ala Gly His Gln Ile Ser Tyr His Arg Val Ser
 370 375 380
 Arg Gly Ser Asn Leu Gln Gln Met Tyr Gly Thr Asn Gln Asn Leu His
 385 390 395 400
 Ser Thr Ser Thr Phe Asp Phe Thr Asn Tyr Asp Ile Tyr Lys Thr Leu

Ser Lys Asp Ala Val Leu Leu Asp Ile Val Tyr Pro Gly Tyr Thr Tyr
 405 410 415
 420 425 430
 Ile Phe Phe Gly Met Pro Glu Val Glu Phe Phe Met Val Asn Gln Leu
 435 440 445
 Asn Asn Thr Arg Lys Thr Leu Lys Tyr Asn Pro Val Ser Lys Asp Ile
 450 455 460
 Ile Ala Ser Thr Arg Asp Ser Glu Leu Glu Leu Pro Pro Glu Thr Ser
 465 470 475 480
 Asp Gln Pro Asn Tyr Glu Ser Tyr Ser His Arg Leu Cys His Ile Thr
 485 490 495
 Ser Ile Pro Ala Thr Gly Asn Thr Thr Gly Leu Val Pro Val Phe Ser
 500 505 510
 Trp Thr His Arg Ser Ala Asp Leu Asn Asn Thr Ile Tyr Ser Asp Lys
 515 520 525
 Ile Thr Gln Ile Pro Ala Val Lys Cys Trp Asp Asn Leu Pro Phe Val
 530 535 540
 Pro Val Val Lys Gly Pro Gly His Thr Gly Gly Asp Leu Leu Gln Tyr
 545 550 555 560
 Asn Arg Ser Thr Gly Ser Val Gly Thr Leu Phe Leu Ala Arg Tyr Gly
 565 570 575
 Leu Ala Leu Glu Lys Ala Gly Lys Tyr Arg Val Arg Leu Arg Tyr Ala
 580 585 590
 Thr Asp Ala Asp Ile Val Leu His Val Asn Asp Ala Gln Ile Gln Met
 595 600 605
 Pro Lys Thr Met Asn Pro Gly Glu Asp Leu Thr Ser Lys Thr Phe Lys
 610 615 620
 Val Ala Asp Ala Ile Thr Thr Val Asn Leu Ala Thr Asp Ser Ser Val
 625 630 635 640
 Ala Val Lys His Asn Leu Gly Glu Asp Pro Asn Ser Thr Leu Ser Gly
 645 650 655
 Ile Val Tyr Val Asp Arg Ile Glu Phe Ile Pro Val Asp Glu Thr Tyr
 660 665 670
 Glu Ala Glu
 675

<210> 81
 <211> 2022
 <212> DNA
 <213> Bacillus thuringiensis (mutated)

<220>
 <221> CDS
 <222> (1)...(2022)

<400> 81
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 1 5 10 15
 tct act tct gta tcc aat gat tct aac aga tac cct ttt gcg aat gag 96
 Ser Thr Ser Val Ser Asn Asp Ser Asn Arg Tyr Pro Phe Ala Asn Glu
 20 25 30
 cca aca aat gcg cta caa aat atg gat tat aaa gat tat tta aaa atg 144
 Pro Thr Asn Ala Leu Gln Asn Met Asp Tyr Lys Asp Tyr Leu Lys Met

35	40	45	
tct gcg gga aat gct agt gaa tac cct ggt tca cct gaa gta ctt gtt			192
Ser Ala Gly Asn Ala Ser Glu Tyr Pro Gly Ser Pro Glu Val Leu Val			
50	55	60	
agc gga caa gat gca gct aag gcc gca att gat ata gta ggt aaa tta			240
Ser Gly Gln Asp Ala Ala Lys Ala Ala Ile Asp Ile Val Gly Lys Leu			
65	70	75	80
cta tca ggt tta ggg gtc cca ttt gtt ggg ccg ata gtg agt ctt tat			288
Leu Ser Gly Leu Gly Val Pro Phe Val Gly Pro Ile Val Ser Leu Tyr			
85	90	95	
act caa ctt att gat att ctg tgg cct tca ggg gaa aag agt caa tgg			336
Thr Gln Leu Ile Asp Ile Leu Trp Pro Ser Gly Glu Lys Ser Gln Trp			
100	105	110	
gaa att ttt atg gaa caa gta gaa gaa ctc att aat caa aaa ata gca			384
Glu Ile Phe Met Glu Gln Val Glu Glu Leu Ile Asn Gln Lys Ile Ala			
115	120	125	
gaa tat gca agg aat aaa gcg ctt tcg gaa tta gaa gga tta ggt aat			432
Glu Tyr Ala Arg Asn Lys Ala Leu Ser Glu Leu Glu Gly Leu Gly Asn			
130	135	140	
aat tac caa tta tat cta act gcg ctt gaa gaa tgg gaa gaa aat cca			480
Asn Tyr Gln Leu Tyr Leu Thr Ala Leu Glu Glu Trp Glu Glu Asn Pro			
145	150	155	160
aat ggt tcc cgg ttt cga agt cga caa gcc tta cga gat gtg cga aat			528
Asn Gly Ser Arg Phe Arg Ser Arg Gln Ala Leu Arg Asp Val Arg Asn			
165	170	175	
cga ttt gaa atc ctg gat agt tta ttt acg caa tat atg cca tct ttt			576
Arg Phe Glu Ile Leu Asp Ser Leu Phe Thr Gln Tyr Met Pro Ser Phe			
180	185	190	
aga gtg aca aat ttt gaa gta cca ttc ctt act gta tat gca atg gca			624
Arg Val Thr Asn Phe Glu Val Pro Phe Leu Thr Val Tyr Ala Met Ala			
195	200	205	
gcc aac ctt cat tta ctg tta tta aag gac gcg tca att ttt gga gaa			672
Ala Asn Leu His Leu Leu Leu Lys Asp Ala Ser Ile Phe Gly Glu			
210	215	220	
gaa tgg gga tgg tca aca act act att aat aac tat tat gat cgt caa			720
Glu Trp Gly Trp Ser Thr Thr Thr Ile Asn Asn Tyr Tyr Asp Arg Gln			
225	230	235	240
atg aaa ctt act gca gaa tat tct gat cac tgt gta aag tgg tat gaa			768
Met Lys Leu Thr Ala Glu Tyr Ser Asp His Cys Val Lys Trp Tyr Glu			
245	250	255	
act ggt tta gca aaa tta aaa ggc acg agc gct aaa caa tgg gtt gac			816
Thr Gly Leu Ala Lys Leu Lys Gly Thr Ser Ala Lys Gln Trp Val Asp			
260	265	270	

tat aac caa ttc cgt aga gaa atg aca ctg gcg gtt tta gat gtt gtt	864
Tyr Asn Gln Phe Arg Arg Glu Met Thr Leu Ala Val Leu Asp Val Val	
275 280 285	
gca tta ttc cca aat tat gac aca cgc acg tac cca atg gaa acg aaa	912
Ala Leu Phe Pro Asn Tyr Asp Thr Arg Thr Tyr Pro Met Glu Thr Lys	
290 295 300	
gca caa cta aca agg gaa gta tat aca gat cca ctg ggc gcg gta aac	960
Ala Gln Leu Thr Arg Glu Val Tyr Thr Asp Pro Leu Gly Ala Val Asn	
305 310 315 320	
gtg tct tca att ggt tcc tgg tat gac aaa gca cct tct ttc gga gtg	1008
Val Ser Ser Ile Gly Ser Trp Tyr Asp Lys Ala Pro Ser Phe Gly Val	
325 330 335	
ata gaa tca tcc gtt att cga cca ccc cat gta ttt gat tat ata acg	1056
Ile Glu Ser Ser Val Ile Arg Pro Pro His Val Phe Asp Tyr Ile Thr	
340 345 350	
gga ctc aca gtg tat aca caa tca aga agc att tct tcc gct cgc tat	1104
Gly Leu Thr Val Tyr Thr Gln Ser Arg Ser Ile Ser Ser Ala Arg Tyr	
355 360 365	
ata aga cat tgg gct ggt cat caa ata agc tac cat cgt gtc agt agg	1152
Ile Arg His Trp Ala Gly His Gln Ile Ser Tyr His Arg Val Ser Arg	
370 375 380	
ggg agt aat ctt caa caa atg tat gga act aat caa aat cta cac agc	1200
Gly Ser Asn Leu Gln Gln Met Tyr Gly Thr Asn Gln Asn Leu His Ser	
385 390 395 400	
act agt acc ttt gat ttt acg aat tat gat att tac aag act cta tca	1248
Thr Ser Thr Phe Asp Phe Thr Asn Tyr Asp Ile Tyr Lys Thr Leu Ser	
405 410 415	
aag gat gca gta ctc ctt gat att gtt tac cct ggt tat acg tat ata	1296
Lys Asp Ala Val Leu Leu Asp Ile Val Tyr Pro Gly Tyr Thr Tyr Ile	
420 425 430	
ttt ttt gga atg cca gaa gtc gag ttt ttc atg gta aac caa ttg aat	1344
Phe Phe Gly Met Pro Glu Val Glu Phe Phe Met Val Asn Gln Leu Asn	
435 440 445	
aat acc aga aag acg tta aag tat aat cca gtt tcc aaa gat att ata	1392
Asn Thr Arg Lys Thr Leu Lys Tyr Asn Pro Val Ser Lys Asp Ile Ile	
450 455 460	
gcg agt aca aga gat tcg gaa tta gaa tta cct cca gaa act tca gat	1440
Ala Ser Thr Arg Asp Ser Glu Leu Glu Leu Pro Pro Glu Thr Ser Asp	
465 470 475 480	
caa cca aat tat gag tca tat agc cat aga tta tgt cat atc aca agt	1488
Gln Pro Asn Tyr Glu Ser Tyr Ser His Arg Leu Cys His Ile Thr Ser	
485 490 495	

att ccc gcg acg ggt aac act acc gga tta gta cct gta ttt tct tgg	1536
Ile Pro Ala Thr Gly Asn Thr Thr Gly Leu Val Pro Val Phe Ser Trp	
500 505 510	
aca cat cga agt gca gat tta aac aat aca ata tat tca gat aaa atc	1584
Thr His Arg Ser Ala Asp Leu Asn Asn Thr Ile Tyr Ser Asp Lys Ile	
515 520 525	
act caa att ccg gcc gtt aaa tgt tgg gat aat tta ccg ttt gtt cca	1632
Thr Gln Ile Pro Ala Val Lys Cys Trp Asp Asn Leu Pro Phe Val Pro	
530 535 540	
gtg gta aaa gga cca gga cat aca gga ggg gat tta tta cag tat aat	1680
Val Val Lys Gly Pro Gly His Thr Gly Gly Asp Leu Leu Gln Tyr Asn	
545 550 555 560	
aga agt act ggt tct gta gga acc tta ttt cta gct cga tat ggc cta	1728
Arg Ser Thr Gly Ser Val Gly Thr Leu Phe Leu Ala Arg Tyr Gly Leu	
565 570 575	
gca tta gaa aaa gca ggg aaa tat cgt gta aga ctg aga tat gct act	1776
Ala Leu Glu Lys Ala Gly Lys Tyr Arg Val Arg Leu Arg Tyr Ala Thr	
580 585 590	
gat gca gat att gta ttg cat gta aac gat gct cag att cag atg cca	1824
Asp Ala Asp Ile Val Leu His Val Asn Asp Ala Gln Ile Gln Met Pro	
595 600 605	
aaa aca atg aac cca ggt gag gat ctg aca tct aaa act ttt aaa gtt	1872
Lys Thr Met Asn Pro Gly Glu Asp Leu Thr Ser Lys Thr Phe Lys Val	
610 615 620	
gca gat gct atc aca aca gtt aat tta gca aca gat agt tcg gtt gca	1920
Ala Asp Ala Ile Thr Thr Val Asn Leu Ala Thr Asp Ser Ser Val Ala	
625 630 635 640	
gtt aaa cat aat tta ggt gaa gac cct aat tca aca tta tct ggt ata	1968
Val Lys His Asn Leu Gly Glu Asp Pro Asn Ser Thr Leu Ser Gly Ile	
645 650 655	
gtt tac gtt gac cga atc gaa ttc atc cca gta gat gag aca tat gaa	2016
Val Tyr Val Asp Arg Ile Glu Phe Ile Pro Val Asp Glu Thr Tyr Glu	
660 665 670	
gcg gaa	2022
Ala Glu	

<210> 82

<211> 674

<212> PRT

<213> *Bacillus thuringiensis* (mutated)

<400> 82

Met	Ser	Pro	Asn	Asn	Gln	Asn	Glu	Tyr	Glu	Ile	Ile	Asp	Ala	Thr	Pro
1				5					10					15	

Ser	Thr	Ser	Val	Ser	Asn	Asp	Ser	Asn	Arg	Tyr	Pro	Phe	Ala	Asn	Glu
			20					25					30		
Pro	Thr	Asn	Ala	Leu	Gln	Asn	Met	Asp	Tyr	Lys	Asp	Tyr	Leu	Lys	Met
		35					40					45			
Ser	Ala	Gly	Asn	Ala	Ser	Glu	Tyr	Pro	Gly	Ser	Pro	Glu	Val	Leu	Val
	50					55					60				
Ser	Gly	Gln	Asp	Ala	Ala	Lys	Ala	Ala	Ile	Asp	Ile	Val	Gly	Lys	Leu
65					70					75					80
Leu	Ser	Gly	Leu	Gly	Val	Pro	Phe	Val	Gly	Pro	Ile	Val	Ser	Leu	Tyr
			85					90						95	
Thr	Gln	Leu	Ile	Asp	Ile	Leu	Trp	Pro	Ser	Gly	Glu	Lys	Ser	Gln	Trp
			100					105						110	
Glu	Ile	Phe	Met	Glu	Gln	Val	Glu	Glu	Leu	Ile	Asn	Gln	Lys	Ile	Ala
		115					120							125	
Glu	Tyr	Ala	Arg	Asn	Lys	Ala	Leu	Ser	Glu	Leu	Glu	Gly	Leu	Gly	Asn
	130					135					140				
Asn	Tyr	Gln	Leu	Tyr	Leu	Thr	Ala	Leu	Glu	Glu	Trp	Glu	Glu	Asn	Pro
145					150					155					160
Asn	Gly	Ser	Arg	Phe	Arg	Ser	Arg	Gln	Ala	Leu	Arg	Asp	Val	Arg	Asn
			165					170						175	
Arg	Phe	Glu	Ile	Leu	Asp	Ser	Leu	Phe	Thr	Gln	Tyr	Met	Pro	Ser	Phe
			180					185						190	
Arg	Val	Thr	Asn	Phe	Glu	Val	Pro	Phe	Leu	Thr	Val	Tyr	Ala	Met	Ala
		195					200					205			
Ala	Asn	Leu	His	Leu	Leu	Leu	Leu	Lys	Asp	Ala	Ser	Ile	Phe	Gly	Glu
	210					215					220				
Glu	Trp	Gly	Trp	Ser	Thr	Thr	Thr	Ile	Asn	Asn	Tyr	Tyr	Asp	Arg	Gln
225					230					235					240
Met	Lys	Leu	Thr	Ala	Glu	Tyr	Ser	Asp	His	Cys	Val	Lys	Trp	Tyr	Glu
			245					250						255	
Thr	Gly	Leu	Ala	Lys	Leu	Lys	Gly	Thr	Ser	Ala	Lys	Gln	Trp	Val	Asp
		260					265						270		
Tyr	Asn	Gln	Phe	Arg	Arg	Glu	Met	Thr	Leu	Ala	Val	Leu	Asp	Val	Val
		275				280						285			
Ala	Leu	Phe	Pro	Asn	Tyr	Asp	Thr	Arg	Thr	Tyr	Pro	Met	Glu	Thr	Lys
	290					295					300				
Ala	Gln	Leu	Thr	Arg	Glu	Val	Tyr	Thr	Asp	Pro	Leu	Gly	Ala	Val	Asn
305					310					315					320
Val	Ser	Ser	Ile	Gly	Ser	Trp	Tyr	Asp	Lys	Ala	Pro	Ser	Phe	Gly	Val
			325					330						335	
Ile	Glu	Ser	Ser	Val	Ile	Arg	Pro	Pro	His	Val	Phe	Asp	Tyr	Ile	Thr
		340					345						350		
Gly	Leu	Thr	Val	Tyr	Thr	Gln	Ser	Arg	Ser	Ile	Ser	Ser	Ala	Arg	Tyr
	355					360						365			
Ile	Arg	His	Trp	Ala	Gly	His	Gln	Ile	Ser	Tyr	His	Arg	Val	Ser	Arg
	370					375					380				
Gly	Ser	Asn	Leu	Gln	Gln	Met	Tyr	Gly	Thr	Asn	Gln	Asn	Leu	His	Ser
385				390						395					400
Thr	Ser	Thr	Phe	Asp	Phe	Thr	Asn	Tyr	Asp	Ile	Tyr	Lys	Thr	Leu	Ser
			405					410						415	
Lys	Asp	Ala	Val	Leu	Leu	Asp	Ile	Val	Tyr	Pro	Gly	Tyr	Thr	Tyr	Ile
		420					425						430		
Phe	Phe	Gly	Met	Pro	Glu	Val	Glu	Phe	Phe	Met	Val	Asn	Gln	Leu	Asn
	435					440					445				
Asn	Thr	Arg	Lys	Thr	Leu	Lys	Tyr	Asn	Pro	Val	Ser	Lys	Asp	Ile	Ile
	450				455					460					
Ala	Ser	Thr	Arg	Asp	Ser	Glu	Leu	Glu	Leu	Pro	Pro	Glu	Thr	Ser	Asp

465		470		475		480									
Gln	Pro	Asn	Tyr	Glu	Ser	Tyr	Ser	His	Arg	Leu	Cys	His	Ile	Thr	Ser
				485					490					495	
Ile	Pro	Ala	Thr	Gly	Asn	Thr	Thr	Gly	Leu	Val	Pro	Val	Phe	Ser	Trp
			500					505					510		
Thr	His	Arg	Ser	Ala	Asp	Leu	Asn	Asn	Thr	Ile	Tyr	Ser	Asp	Lys	Ile
		515					520				525				
Thr	Gln	Ile	Pro	Ala	Val	Lys	Cys	Trp	Asp	Asn	Leu	Pro	Phe	Val	Pro
	530					535				540					
Val	Val	Lys	Gly	Pro	Gly	His	Thr	Gly	Gly	Asp	Leu	Leu	Gln	Tyr	Asn
545					550					555					560
Arg	Ser	Thr	Gly	Ser	Val	Gly	Thr	Leu	Phe	Leu	Ala	Arg	Tyr	Gly	Leu
			565						570					575	
Ala	Leu	Glu	Lys	Ala	Gly	Lys	Tyr	Arg	Val	Arg	Leu	Arg	Tyr	Ala	Thr
			580					585					590		
Asp	Ala	Asp	Ile	Val	Leu	His	Val	Asn	Asp	Ala	Gln	Ile	Gln	Met	Pro
	595						600				605				
Lys	Thr	Met	Asn	Pro	Gly	Glu	Asp	Leu	Thr	Ser	Lys	Thr	Phe	Lys	Val
	610					615					620				
Ala	Asp	Ala	Ile	Thr	Thr	Val	Asn	Leu	Ala	Thr	Asp	Ser	Ser	Val	Ala
625					630					635					640
Val	Lys	His	Asn	Leu	Gly	Glu	Asp	Pro	Asn	Ser	Thr	Leu	Ser	Gly	Ile
			645						650					655	
Val	Tyr	Val	Asp	Arg	Ile	Glu	Phe	Ile	Pro	Val	Asp	Glu	Thr	Tyr	Glu
			660					665					670		
Ala	Glu														

<210> 83
 <211> 2031
 <212> DNA
 <213> *Bacillus thuringiensis*

<220>
 <221> CDS
 <222> (1)...(2031)

<400> 83	
atg agt cca aat aat caa aat gaa tat gaa att ata gat gcg aca cct	48
Met Ser Pro Asn Asn Gln Asn Glu Tyr Glu Ile Ile Asp Ala Thr Pro	
1 5 10 15	
tct act tct gta tcc aat gat tct aac aga tac cct ttt gcg aat gag	96
Ser Thr Ser Val Ser Asn Asp Ser Asn Arg Tyr Pro Phe Ala Asn Glu	
20 25 30	
cca aca aat gcg cta caa aat atg gat tat aaa gat tat tta aaa atg	144
Pro Thr Asn Ala Leu Gln Asn Met Asp Tyr Lys Asp Tyr Leu Lys Met	
35 40 45	
tct gcg gga aat gct agt gaa tac cct ggt tca cct gaa gta ctt gtt	192
Ser Ala Gly Asn Ala Ser Glu Tyr Pro Gly Ser Pro Glu Val Leu Val	
50 55 60	
agc gga caa gat gca gct aag gcc gca att gat ata gta ggt aaa tta	240
Ser Gly Gln Asp Ala Ala Lys Ala Ala Ile Asp Ile Val Gly Lys Leu	

65	70	75	80	
cta tca ggt tta ggg gtc cca ttt gtt ggg ccg ata gtg agt ctt tat				288
Leu Ser Gly Leu Gly Val Pro Phe Val Gly Pro Ile Val Ser Leu Tyr	85	90	95	
act caa ctt att gat att ctg tgg cct tca ggg gaa aag agt caa tgg				336
Thr Gln Leu Ile Asp Ile Leu Trp Pro Ser Gly Glu Lys Ser Gln Trp	100	105	110	
gaa att ttt atg gaa caa gta gaa gaa ctc att aat caa aaa ata gca				384
Glu Ile Phe Met Glu Gln Val Glu Glu Leu Ile Asn Gln Lys Ile Ala	115	120	125	
gaa tat gca agg aat aaa gcg ctt tcg gaa tta gaa gga tta ggt aat				432
Glu Tyr Ala Arg Asn Lys Ala Leu Ser Glu Leu Glu Gly Leu Gly Asn	130	135	140	
aat tac caa tta tat cta act gcg ctt gaa gaa tgg gaa gaa aat cca				480
Asn Tyr Gln Leu Tyr Leu Thr Ala Leu Glu Glu Trp Glu Glu Asn Pro	145	150	155	160
ttt cga agt cga ggt agt tta aat ggt tcc cgg cca gcc tta cga gat				528
Phe Arg Ser Arg Gly Ser Leu Asn Gly Ser Arg Pro Ala Leu Arg Asp	165	170	175	
gtg cga aat cga ttt gaa atc ctg gat agt tta ttt acg caa tat atg				576
Val Arg Asn Arg Phe Glu Ile Leu Asp Ser Leu Phe Thr Gln Tyr Met	180	185	190	
cca tct ttt aga gtg aca aat ttt gaa gta cca ttc ctt act gta tat				624
Pro Ser Phe Arg Val Thr Asn Phe Glu Val Pro Phe Leu Thr Val Tyr	195	200	205	
gca atg gca gcc aac ctt cat tta ctg tta tta aag gac gcg tca att				672
Ala Met Ala Ala Asn Leu His Leu Leu Leu Leu Lys Asp Ala Ser Ile	210	215	220	
ttt gga gaa gaa tgg gga tgg tca aca act act att aat aac tat tat				720
Phe Gly Glu Glu Trp Gly Trp Ser Thr Thr Thr Ile Asn Asn Tyr Tyr	225	230	235	240
gat cgt caa atg aaa ctt act gca gaa tat tct gat cac tgt gta aag				768
Asp Arg Gln Met Lys Leu Thr Ala Glu Tyr Ser Asp His Cys Val Lys	245	250	255	
tgg tat gaa act ggt tta gca aaa tta aaa ggc acg agc gct aaa caa				816
Trp Tyr Glu Thr Gly Leu Ala Lys Leu Lys Gly Thr Ser Ala Lys Gln	260	265	270	
tgg gtt gac tat aac caa ttc cgt aga gaa atg aca ctg gcg gtt tta				864
Trp Val Asp Tyr Asn Gln Phe Arg Arg Glu Met Thr Leu Ala Val Leu	275	280	285	
gat gtt gtt gca tta ttc cca aat tat gac aca cgc acg tac cca atg				912
Asp Val Val Ala Leu Phe Pro Asn Tyr Asp Thr Arg Thr Tyr Pro Met	290	295	300	

gaa acg aaa gca caa cta aca agg gaa gta tat aca gat cca ctg ggc Glu Thr Lys Ala Gln Leu Thr Arg Glu Val Tyr Thr Asp Pro Leu Gly 305 310 315 320	960
gcg gta aac gtg tct tca att ggt tcc tgg tat gac aaa gca cct tct Ala Val Asn Val Ser Ser Ile Gly Ser Trp Tyr Asp Lys Ala Pro Ser 325 330 335	1008
ttc gga gtg ata gaa tca tcc gtt att cga cca ccc cat gta ttt gat Phe Gly Val Ile Glu Ser Ser Val Ile Arg Pro Pro His Val Phe Asp 340 345 350	1056
tat ata acg gga ctc aca gtg tat aca caa tca aga agc att tct tcc Tyr Ile Thr Gly Leu Thr Val Tyr Thr Gln Ser Arg Ser Ile Ser Ser 355 360 365	1104
gct cgc tat ata aga cat tgg gct ggt cat caa ata agc tac cat cgt Ala Arg Tyr Ile Arg His Trp Ala Gly His Gln Ile Ser Tyr His Arg 370 375 380	1152
gtc agt agg ggt agt aat ctt caa caa atg tat gga act aat caa aat Val Ser Arg Gly Ser Asn Leu Gln Gln Met Tyr Gly Thr Asn Gln Asn 385 390 395 400	1200
cta cac agc act agt acc ttt gat ttt acg aat tat gat att tac aag Leu His Ser Thr Ser Thr Phe Asp Phe Thr Asn Tyr Asp Ile Tyr Lys 405 410 415	1248
act cta tca aag gat gca gta ctc ctt gat att gtt tac cct ggt tat Thr Leu Ser Lys Asp Ala Val Leu Leu Asp Ile Val Tyr Pro Gly Tyr 420 425 430	1296
acg tat ata ttt ttt gga atg cca gaa gtc gag ttt ttc atg gta aac Thr Tyr Ile Phe Phe Gly Met Pro Glu Val Glu Phe Phe Met Val Asn 435 440 445	1344
caa ttg aat aat acc aga aag acg tta aag tat aat cca gtt tcc aaa Gln Leu Asn Asn Thr Arg Lys Thr Leu Lys Tyr Asn Pro Val Ser Lys 450 455 460	1392
gat att ata gcg agt aca aga gat tcg gaa tta gaa tta cct cca gaa Asp Ile Ile Ala Ser Thr Arg Asp Ser Glu Leu Glu Leu Pro Pro Glu 465 470 475 480	1440
act tca gat caa cca aat tat gag tca tat agc cat aga tta tgt cat Thr Ser Asp Gln Pro Asn Tyr Glu Ser Tyr Ser His Arg Leu Cys His 485 490 495	1488
atc aca agt att ccc gcg acg ggt aac act acc gga tta gta cct gta Ile Thr Ser Ile Pro Ala Thr Gly Asn Thr Thr Gly Leu Val Pro Val 500 505 510	1536
ttt tct tgg aca cat cga agt gca gat tta aac aat aca ata tat tca Phe Ser Trp Thr His Arg Ser Ala Asp Leu Asn Asn Thr Ile Tyr Ser 515 520 525	1584

gat aaa atc act caa att ccg gcc gtt aaa tgt tgg gat aat tta ccg	1632
Asp Lys Ile Thr Gln Ile Pro Ala Val Lys Cys Trp Asp Asn Leu Pro	
530 535 540	
ttt gtt cca gtg gta aaa gga cca gga cat aca gga ggg gat tta tta	1680
Phe Val Pro Val Val Lys Gly Pro Gly His Thr Gly Gly Asp Leu Leu	
545 550 555 560	
cag tat aat aga agt act ggt tct gta gga acc tta ttt cta gct cga	1728
Gln Tyr Asn Arg Ser Thr Gly Ser Val Gly Thr Leu Phe Leu Ala Arg	
565 570 575	
tat ggc cta gca tta gaa aaa gca ggg aaa tat cgt gta aga ctg aga	1776
Tyr Gly Leu Ala Leu Glu Lys Ala Gly Lys Tyr Arg Val Arg Leu Arg	
580 585 590	
tat gct act gat gca gat att gta ttg cat gta aac gat gct cag att	1824
Tyr Ala Thr Asp Ala Asp Ile Val Leu His Val Asn Asp Ala Gln Ile	
595 600 605	
cag atg cca aaa aca atg aac cca ggt gag gat ctg aca tct aaa act	1872
Gln Met Pro Lys Thr Met Asn Pro Gly Glu Asp Leu Thr Ser Lys Thr	
610 615 620	
ttt aaa gtt gca gat gct atc aca aca gtt aat tta gca aca gat agt	1920
Phe Lys Val Ala Asp Ala Ile Thr Thr Val Asn Leu Ala Thr Asp Ser	
625 630 635 640	
tcg gtt gca gtt aaa cat aat tta ggt gaa gac cct aat tca aca tta	1968
Ser Val Ala Val Lys His Asn Leu Gly Glu Asp Pro Asn Ser Thr Leu	
645 650 655	
tct ggt ata gtt tac gtt gac cga atc gaa ttc atc cca gta gat gag	2016
Ser Gly Ile Val Tyr Val Asp Arg Ile Glu Phe Ile Pro Val Asp Glu	
660 665 670	
aca tat gaa gcg gaa	2031
Thr Tyr Glu Ala Glu	
675	

<210> 84
 <211> 677
 <212> PRT
 <213> Bacillus thuringiensis

<400> 84
Met Ser Pro Asn Asn Gln Asn Glu Tyr Glu Ile Ile Asp Ala Thr Pro
1 5 10 15
Ser Thr Ser Val Ser Asn Asp Ser Asn Arg Tyr Pro Phe Ala Asn Glu
20 25 30
Pro Thr Asn Ala Leu Gln Asn Met Asp Tyr Lys Asp Tyr Leu Lys Met
35 40 45
Ser Ala Gly Asn Ala Ser Glu Tyr Pro Gly Ser Pro Glu Val Leu Val
50 55 60
Ser Gly Gln Asp Ala Ala Lys Ala Ala Ile Asp Ile Val Gly Lys Leu
65 70 75 80

Leu Ser Gly Leu Gly Val Pro Phe Val Gly Pro Ile Val Ser Leu Tyr
 85 90 95
 Thr Gln Leu Ile Asp Ile Leu Trp Pro Ser Gly Glu Lys Ser Gln Trp
 100 105 110
 Glu Ile Phe Met Glu Gln Val Glu Glu Leu Ile Asn Gln Lys Ile Ala
 115 120 125
 Glu Tyr Ala Arg Asn Lys Ala Leu Ser Glu Leu Glu Gly Leu Gly Asn
 130 135 140
 Asn Tyr Gln Leu Tyr Leu Thr Ala Leu Glu Glu Trp Glu Glu Asn Pro
 145 150 155 160
 Phe Arg Ser Arg Gly Ser Leu Asn Gly Ser Arg Pro Ala Leu Arg Asp
 165 170 175
 Val Arg Asn Arg Phe Glu Ile Leu Asp Ser Leu Phe Thr Gln Tyr Met
 180 185 190
 Pro Ser Phe Arg Val Thr Asn Phe Glu Val Pro Phe Leu Thr Val Tyr
 195 200 205
 Ala Met Ala Ala Asn Leu His Leu Leu Leu Lys Asp Ala Ser Ile
 210 215 220
 Phe Gly Glu Glu Trp Gly Trp Ser Thr Thr Thr Ile Asn Asn Tyr Tyr
 225 230 235 240
 Asp Arg Gln Met Lys Leu Thr Ala Glu Tyr Ser Asp His Cys Val Lys
 245 250 255
 Trp Tyr Glu Thr Gly Leu Ala Lys Leu Lys Gly Thr Ser Ala Lys Gln
 260 265 270
 Trp Val Asp Tyr Asn Gln Phe Arg Arg Glu Met Thr Leu Ala Val Leu
 275 280 285
 Asp Val Val Ala Leu Phe Pro Asn Tyr Asp Thr Arg Thr Tyr Pro Met
 290 295 300
 Glu Thr Lys Ala Gln Leu Thr Arg Glu Val Tyr Thr Asp Pro Leu Gly
 305 310 315 320
 Ala Val Asn Val Ser Ser Ile Gly Ser Trp Tyr Asp Lys Ala Pro Ser
 325 330 335
 Phe Gly Val Ile Glu Ser Ser Val Ile Arg Pro Pro His Val Phe Asp
 340 345 350
 Tyr Ile Thr Gly Leu Thr Val Tyr Thr Gln Ser Arg Ser Ile Ser Ser
 355 360 365
 Ala Arg Tyr Ile Arg His Trp Ala Gly His Gln Ile Ser Tyr His Arg
 370 375 380
 Val Ser Arg Gly Ser Asn Leu Gln Gln Met Tyr Gly Thr Asn Gln Asn
 385 390 395 400
 Leu His Ser Thr Ser Thr Phe Asp Phe Thr Asn Tyr Asp Ile Tyr Lys
 405 410 415
 Thr Leu Ser Lys Asp Ala Val Leu Leu Asp Ile Val Tyr Pro Gly Tyr
 420 425 430
 Thr Tyr Ile Phe Phe Gly Met Pro Glu Val Glu Phe Phe Met Val Asn
 435 440 445
 Gln Leu Asn Asn Thr Arg Lys Thr Leu Lys Tyr Asn Pro Val Ser Lys
 450 455 460
 Asp Ile Ile Ala Ser Thr Arg Asp Ser Glu Leu Glu Leu Pro Pro Glu
 465 470 475 480
 Thr Ser Asp Gln Pro Asn Tyr Glu Ser Tyr Ser His Arg Leu Cys His
 485 490 495
 Ile Thr Ser Ile Pro Ala Thr Gly Asn Thr Thr Gly Leu Val Pro Val
 500 505 510
 Phe Ser Trp Thr His Arg Ser Ala Asp Leu Asn Asn Thr Ile Tyr Ser
 515 520 525
 Asp Lys Ile Thr Gln Ile Pro Ala Val Lys Cys Trp Asp Asn Leu Pro

530		535		540
Phe Val Pro Val Val	Lys Gly Pro Gly His Thr	Gly Gly Asp Leu Leu		
545	550	555	560	
Gln Tyr Asn Arg Ser Thr	Gly Ser Val Gly Thr	Leu Phe Leu Ala Arg		
	565	570	575	
Tyr Gly Leu Ala Leu	Glu Lys Ala Gly Lys Tyr	Arg Val Arg Leu Arg		
	580	585	590	
Tyr Ala Thr Asp Ala	Asp Ile Val Leu His Val	Asn Asp Ala Gln Ile		
	595	600	605	
Gln Met Pro Lys Thr	Met Asn Pro Gly Glu Asp	Leu Thr Ser Lys Thr		
	610	615	620	
Phe Lys Val Ala Asp	Ala Ile Thr Thr Val	Asn Leu Ala Thr Asp Ser		
625	630	635	640	
Ser Val Ala Val Lys	His Asn Leu Gly Glu	Asp Pro Asn Ser Thr Leu		
	645	650	655	
Ser Gly Ile Val Tyr	Val Asp Arg Ile Glu	Phe Ile Pro Val Asp Glu		
	660	665	670	
Thr Tyr Glu Ala Glu				
675				

<210> 85
 <211> 2019
 <212> DNA
 <213> *Bacillus thuringiensis* (mutated)

<220>
 <221> CDS
 <222> (1) ... (2019)

<400> 85	
atg agt cca aat aat caa aat gaa tat gaa att ata gat gcg aca cct	48
Met Ser Pro Asn Asn Gln Asn Glu Tyr Glu Ile Ile Asp Ala Thr Pro	
1 5 10 15	
tct act tct gta tcc aat gat tct aac aga tac cct ttt gcg aat gag	96
Ser Thr Ser Val Ser Asn Asp Ser Asn Arg Tyr Pro Phe Ala Asn Glu	
20 25 30	
cca aca aat gcg cta caa aat atg gat tat aaa gat tat gca gta ggg	144
Pro Thr Asn Ala Leu Gln Asn Met Asp Tyr Lys Asp Tyr Ala Val Gly	
35 40 45	
tct gcg gga aat gct agt gaa tac cct ggt tca cct gaa gta ctt gtt	192
Ser Ala Gly Asn Ala Ser Glu Tyr Pro Gly Ser Pro Glu Val Leu Val	
50 55 60	
agc gga caa gat gca gct aag gcc gca att gat ata gta ggt aaa tta	240
Ser Gly Gln Asp Ala Ala Lys Ala Ala Ile Asp Ile Val Gly Lys Leu	
65 70 75 80	
cta tca ggt tta ggg gtc cca ttt gtt ggg ccg ata gtg agt ctt tat	288
Leu Ser Gly Leu Gly Val Pro Phe Val Gly Pro Ile Val Ser Leu Tyr	
85 90 95	
act caa ctt att gat att ctg tgg cct tca ggg gaa aag agt caa tgg	336
Thr Gln Leu Ile Asp Ile Leu Trp Pro Ser Gly Glu Lys Ser Gln Trp	

100	105	110	
gaa att ttt atg gaa caa gta	gaa gaa ctc att aat caa aaa ata gca	384	
Glu Ile Phe Met Glu Gln Val	Glu Glu Leu Ile Asn Gln Lys Ile Ala		
115	120 125		
gaa tat gca agg aat aaa gcg ctt tcg gaa tta gaa gga tta ggt aat	432		
Glu Tyr Ala Arg Asn Lys Ala Leu Ser Glu Leu Glu Gly Leu Gly Asn			
130 135	140		
aat tac caa tta tat cta act gcg ctt gaa gaa tgg gaa gaa aat cca	480		
Asn Tyr Gln Leu Tyr Leu Thr Ala Leu Glu Glu Trp Glu Glu Asn Pro			
145 150 155	160		
ttt cga cga ggt ttt cga cga ggt gcc tta cga gat gtg cga aat cga	528		
Phe Arg Arg Gly Phe Arg Arg Gly Ala Leu Arg Asp Val Arg Asn Arg			
165 170 175			
ttt gaa atc ctg gat agt tta ttt acg caa tat atg cca tct ttt aga	576		
Phe Glu Ile Leu Asp Ser Leu Phe Thr Gln Tyr Met Pro Ser Phe Arg			
180 185	190		
gtg aca aat ttt gaa gta cca ttc ctt act gta tat gca atg gca gcc	624		
Val Thr Asn Phe Glu Val Pro Phe Leu Thr Val Tyr Ala Met Ala Ala			
195 200	205		
aac ctt cat tta ctg tta tta aag gac gcg tca att ttt gga gaa gaa	672		
Asn Leu His Leu Leu Leu Leu Lys Asp Ala Ser Ile Phe Gly Glu Glu			
210 215	220		
tgg gga tgg tca aca act act att aat aac gtg gtg gat cgt caa atg	720		
Trp Gly Trp Ser Thr Thr Thr Ile Asn Asn Val Val Asp Arg Gln Met			
225 230 235	240		
aaa ctt act gca gaa tat tct gat cac tgt gta aag tgg tat gaa act	768		
Lys Leu Thr Ala Glu Tyr Ser Asp His Cys Val Lys Trp Tyr Glu Thr			
245 250	255		
ggt tta gca aaa tta aaa ggc acg agc gct aaa caa tgg gtt gac tat	816		
Gly Leu Ala Lys Leu Lys Gly Thr Ser Ala Lys Gln Trp Val Asp Tyr			
260 265	270		
aac caa ttc cgt aga gaa atg aca ctg gcg gtt tta gat gtt gtt gca	864		
Asn Gln Phe Arg Arg Glu Met Thr Leu Ala Val Leu Asp Val Val Ala			
275 280	285		
tta ttc cca aat tat gac aca ata acg tac cca ata gaa acg aaa gca	912		
Leu Phe Pro Asn Tyr Asp Thr Ile Thr Tyr Pro Ile Glu Thr Lys Ala			
290 295	300		
caa cta aca agg gaa gta tat aca gat cca ctg ggc gcg gta aac gtg	960		
Gln Leu Thr Arg Glu Val Tyr Thr Asp Pro Leu Gly Ala Val Asn Val			
305 310 315	320		
tct tca att ggt tcc tgg tat gac aaa gca cct tct ttc gga gtg ata	1008		
Ser Ser Ile Gly Ser Trp Tyr Asp Lys Ala Pro Ser Phe Gly Val Ile			
325 330	335		

gaa tca tcc gtt att cga cca ccc cat gta ttt gat tat ata acg gga	1056
Glu Ser Ser Val Ile Arg Pro Pro His Val Phe Asp Tyr Ile Thr Gly	
340 345 350	
ctc aca gtg tat aca caa tca aga agc att tct tcc gct cgc tat ata	1104
Leu Thr Val Tyr Thr Gln Ser Arg Ser Ile Ser Ser Ala Arg Tyr Ile	
355 360 365	
aga cat tgg gct ggt cat caa ata agc tac cat cgt gtc agt agg ggt	1152
Arg His Trp Ala Gly His Gln Ile Ser Tyr His Arg Val Ser Arg Gly	
370 375 380	
agt aat ctt caa caa atg tat gga act aat caa aat cta cac agc act	1200
Ser Asn Leu Gln Gln Met Tyr Gly Thr Asn Gln Asn Leu His Ser Thr	
385 390 395 400	
agt acc ttt gat ttt acg aat tat gat att tac aag act cta tca aag	1248
Ser Thr Phe Asp Phe Thr Asn Tyr Asp Ile Tyr Lys Thr Leu Ser Lys	
405 410 415	
gat gca gta ctc ctt gat att gtt tac cct ggt tat acg tat ata ttt	1296
Asp Ala Val Leu Leu Asp Ile Val Tyr Pro Gly Tyr Thr Tyr Ile Phe	
420 425 430	
ttt gga atg cca gaa gtc gag ttt ttc atg gta aac caa ttg aat aat	1344
Phe Gly Met Pro Glu Val Glu Phe Phe Met Val Asn Gln Leu Asn Asn	
435 440 445	
acc aga aag acg tta aag tat aat cca gtt tcc aaa gat att ata gcg	1392
Thr Arg Lys Thr Leu Lys Tyr Asn Pro Val Ser Lys Asp Ile Ile Ala	
450 455 460	
agt aca aga gat tcg gaa tta gaa tta cct cca gaa act tca gat caa	1440
Ser Thr Arg Asp Ser Glu Leu Glu Leu Pro Pro Glu Thr Ser Asp Gln	
465 470 475 480	
cca aat tat gag tca tat agc cat aga tta tgt cat atc aca agt att	1488
Pro Asn Tyr Glu Ser Tyr Ser His Arg Leu Cys His Ile Thr Ser Ile	
485 490 495	
ccc gcg acg ggt aac act acc gga tta gta cct gta ttt tct tgg aca	1536
Pro Ala Thr Gly Asn Thr Thr Gly Leu Val Pro Val Phe Ser Trp Thr	
500 505 510	
cat cga agt gca gat tta aac aat aca ata tat tca gat aaa atc act	1584
His Arg Ser Ala Asp Leu Asn Asn Thr Ile Tyr Ser Asp Lys Ile Thr	
515 520 525	
caa att ccg gcc gtt aaa tgt tgg gat aat tta ccg ttt gtt cca gtg	1632
Gln Ile Pro Ala Val Lys Cys Trp Asp Asn Leu Pro Phe Val Pro Val	
530 535 540	
gta aaa gga cca gga cat aca gga ggg gat tta tta cag tat aat aga	1680
Val Lys Gly Pro Gly His Thr Gly Gly Asp Leu Leu Gln Tyr Asn Arg	
545 550 555 560	

agt act ggt tct gta gga acc tta ttt cta gct cga tat ggc cta gca	1728
Ser Thr Gly Ser Val Gly Thr Leu Phe Leu Ala Arg Tyr Gly Leu Ala	
565 570 575	
tta gaa aaa gca ggg aaa tat cgt gta aga ctg aga tat gct act gat	1776
Leu Glu Lys Ala Gly Lys Tyr Arg Val Arg Leu Arg Tyr Ala Thr Asp	
580 585 590	
gca gat att gta ttg cat gta aac gat gct cag att cag atg cca aaa	1824
Ala Asp Ile Val Leu His Val Asn Asp Ala Gln Ile Gln Met Pro Lys	
595 600 605	
aca atg aac cca ggt gag gat ctg aca tct aaa act ttt aaa gtt gca	1872
Thr Met Asn Pro Gly Glu Asp Leu Thr Ser Lys Thr Phe Lys Val Ala	
610 615 620	
gat gct atc aca aca gtt aat tta gca aca gat agt tcg gtt gca gtt	1920
Asp Ala Ile Thr Thr Val Asn Leu Ala Thr Asp Ser Ser Val Ala Val	
625 630 635 640	
aaa cat aat tta ggt gaa gac cct aat tca aca tta tct ggt ata gtt	1968
Lys His Asn Leu Gly Glu Asp Pro Asn Ser Thr Leu Ser Gly Ile Val	
645 650 655	
tac gtt gac cga atc gaa ttc atc cca gta gat gag aca tat gaa gcg	2016
Tyr Val Asp Arg Ile Glu Phe Ile Pro Val Asp Glu Thr Tyr Glu Ala	
660 665 670	
gaa	2019
Glu	

<210> 86
 <211> 673
 <212> PRT
 <213> Bacillus thuringiensis (mutated)

<400> 86

Met Ser Pro Asn Asn Gln Asn Glu Tyr Glu Ile Ile Asp Ala Thr Pro	
1 5 10 15	
Ser Thr Ser Val Ser Asn Asp Ser Asn Arg Tyr Pro Phe Ala Asn Glu	
20 25 30	
Pro Thr Asn Ala Leu Gln Asn Met Asp Tyr Lys Asp Tyr Ala Val Gly	
35 40 45	
Ser Ala Gly Asn Ala Ser Glu Tyr Pro Gly Ser Pro Glu Val Leu Val	
50 55 60	
Ser Gly Gln Asp Ala Ala Lys Ala Ala Ile Asp Ile Val Gly Lys Leu	
65 70 75 80	
Leu Ser Gly Leu Gly Val Pro Phe Val Gly Pro Ile Val Ser Leu Tyr	
85 90 95	
Thr Gln Leu Ile Asp Ile Leu Trp Pro Ser Gly Glu Lys Ser Gln Trp	
100 105 110	
Glu Ile Phe Met Glu Gln Val Glu Glu Leu Ile Asn Gln Lys Ile Ala	
115 120 125	
Glu Tyr Ala Arg Asn Lys Ala Leu Ser Glu Leu Glu Gly Leu Gly Asn	
130 135 140	

Asn	Tyr	Gln	Leu	Tyr	Leu	Thr	Ala	Leu	Glu	Glu	Trp	Glu	Glu	Asn	Pro	145	150	155	160
Phe	Arg	Arg	Gly	Phe	Arg	Arg	Gly	Ala	Leu	Arg	Asp	Val	Arg	Asn	Arg	165	170		175
Phe	Glu	Ile	Leu	Asp	Ser	Leu	Phe	Thr	Gln	Tyr	Met	Pro	Ser	Phe	Arg	180	185		190
Val	Thr	Asn	Phe	Glu	Val	Pro	Phe	Leu	Thr	Val	Tyr	Ala	Met	Ala	Ala	195	200		205
Asn	Leu	His	Leu	Leu	Leu	Leu	Lys	Asp	Ala	Ser	Ile	Phe	Gly	Glu	Glu	210	215		220
Trp	Gly	Trp	Ser	Thr	Thr	Thr	Ile	Asn	Asn	Val	Val	Asp	Arg	Gln	Met	225	230		235
Lys	Leu	Thr	Ala	Glu	Tyr	Ser	Asp	His	Cys	Val	Lys	Trp	Tyr	Glu	Thr	245	250		255
Gly	Leu	Ala	Lys	Leu	Lys	Gly	Thr	Ser	Ala	Lys	Gln	Trp	Val	Asp	Tyr	260	265		270
Asn	Gln	Phe	Arg	Arg	Glu	Met	Thr	Leu	Ala	Val	Leu	Asp	Val	Val	Ala	275	280		285
Leu	Phe	Pro	Asn	Tyr	Asp	Thr	Ile	Thr	Tyr	Pro	Ile	Glu	Thr	Lys	Ala	290	295		300
Gln	Leu	Thr	Arg	Glu	Val	Tyr	Thr	Asp	Pro	Leu	Gly	Ala	Val	Asn	Val	305	310		315
Ser	Ser	Ile	Gly	Ser	Trp	Tyr	Asp	Lys	Ala	Pro	Ser	Phe	Gly	Val	Ile	325	330		335
Glu	Ser	Ser	Val	Ile	Arg	Pro	Pro	His	Val	Phe	Asp	Tyr	Ile	Thr	Gly	340	345		350
Leu	Thr	Val	Tyr	Thr	Gln	Ser	Arg	Ser	Ile	Ser	Ser	Ala	Arg	Tyr	Ile	355	360		365
Arg	His	Trp	Ala	Gly	His	Gln	Ile	Ser	Tyr	His	Arg	Val	Ser	Arg	Gly	370	375		380
Ser	Asn	Leu	Gln	Gln	Met	Tyr	Gly	Thr	Asn	Gln	Asn	Leu	His	Ser	Thr	385	390		395
Ser	Thr	Phe	Asp	Phe	Thr	Asn	Tyr	Asp	Ile	Tyr	Lys	Thr	Leu	Ser	Lys	405	410		415
Asp	Ala	Val	Leu	Leu	Asp	Ile	Val	Tyr	Pro	Gly	Tyr	Thr	Tyr	Ile	Phe	420	425		430
Phe	Gly	Met	Pro	Glu	Val	Glu	Phe	Phe	Met	Val	Asn	Gln	Leu	Asn	Asn	435	440		445
Thr	Arg	Lys	Thr	Leu	Lys	Tyr	Asn	Pro	Val	Ser	Lys	Asp	Ile	Ile	Ala	450	455		460
Ser	Thr	Arg	Asp	Ser	Glu	Leu	Glu	Leu	Pro	Pro	Glu	Thr	Ser	Asp	Gln	465	470		475
Pro	Asn	Tyr	Glu	Ser	Tyr	Ser	His	Arg	Leu	Cys	His	Ile	Thr	Ser	Ile	485	490		495
Pro	Ala	Thr	Gly	Asn	Thr	Thr	Gly	Leu	Val	Pro	Val	Phe	Ser	Trp	Thr	500	505		510
His	Arg	Ser	Ala	Asp	Leu	Asn	Asn	Thr	Ile	Tyr	Ser	Asp	Lys	Ile	Thr	515	520		525
Gln	Ile	Pro	Ala	Val	Lys	Cys	Trp	Asp	Asn	Leu	Pro	Phe	Val	Pro	Val	530	535		540
Val	Lys	Gly	Pro	Gly	His	Thr	Gly	Gly	Asp	Leu	Leu	Gln	Tyr	Asn	Arg	545	550		555
Ser	Thr	Gly	Ser	Val	Gly	Thr	Leu	Phe	Leu	Ala	Arg	Tyr	Gly	Leu	Ala	565	570		575
Leu	Glu	Lys	Ala	Gly	Lys	Tyr	Arg	Val	Arg	Leu	Arg	Tyr	Ala	Thr	Asp	580	585		590
Ala	Asp	Ile	Val	Leu	His	Val	Asn	Asp	Ala	Gln	Ile	Gln	Met	Pro	Lys				

595 600 605
 Thr Met Asn Pro Gly Glu Asp Leu Thr Ser Lys Thr Phe Lys Val Ala
 610 615 620
 Asp Ala Ile Thr Thr Val Asn Leu Ala Thr Asp Ser Ser Val Ala Val
 625 630 635 640
 Lys His Asn Leu Gly Glu Asp Pro Asn Ser Thr Leu Ser Gly Ile Val
 645 650 655
 Tyr Val Asp Arg Ile Glu Phe Ile Pro Val Asp Glu Thr Tyr Glu Ala
 660 665 670
 Glu

<210> 87
 <211> 2019
 <212> DNA
 <213> *Bacillus thuringiensis* (mutated)

<220>
 <221> CDS
 <222> (1)...(2019)

<400> 87
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 Met Ser Pro Asn Asn Gln Asn Glu Tyr Glu Ile Ile Asp Ala Thr Pro
 1 5 10 15

 tct act tct gta tcc aat gat tct aac aga tac cct ttt gcg aat gag 96
 Ser Thr Ser Val Ser Asn Asp Ser Asn Arg Tyr Pro Phe Ala Asn Glu
 20 25 30

 cca aca aat gcg cta caa aat atg gat tat aaa gat tat gca gta ggg 144
 Pro Thr Asn Ala Leu Gln Asn Met Asp Tyr Lys Asp Tyr Ala Val Gly
 35 40 45

 tct gcg gga aat gct agt gaa tac cct ggt tca cct gaa gta ctt gtt 192
 Ser Ala Gly Asn Ala Ser Glu Tyr Pro Gly Ser Pro Glu Val Leu Val
 50 55 60

 agc gga caa gat gca gct aag gcc gca att gat ata gta ggt aaa tta 240
 Ser Gly Gln Asp Ala Ala Lys Ala Ala Ile Asp Ile Val Gly Lys Leu
 65 70 75 80

 cta tca ggt tta ggg gtc cca ttt gtt ggg ccg ata gtg agt ctt tat 288
 Leu Ser Gly Leu Gly Val Pro Phe Val Gly Pro Ile Val Ser Leu Tyr
 85 90 95

 act caa ctt att gat att ctg tgg cct tca ggg gaa aag agt caa tgg 336
 Thr Gln Leu Ile Asp Ile Leu Trp Pro Ser Gly Glu Lys Ser Gln Trp
 100 105 110

 gaa att ttt atg gaa caa gta gaa gaa ctc att aat caa aaa ata gca 384
 Glu Ile Phe Met Glu Gln Val Glu Glu Leu Ile Asn Gln Lys Ile Ala
 115 120 125

 gaa tat gca agg aat aaa gcg ctt tcg gaa tta gaa gga tta ggt aat 432
 Glu Tyr Ala Arg Asn Lys Ala Leu Ser Glu Leu Glu Gly Leu Gly Asn

130	135	140	
aat tac caa tta tat cta act gcg ctt gaa gaa tgg gaa gaa aat cca			480
Asn Tyr Gln Leu Tyr Leu Thr Ala Leu Glu Glu Trp Glu Glu Asn Pro			
145	150	155	160
ttt cga cga ggt ttt cga cga ggt gcc tta cga gat gtg cga aat cga			528
Phe Arg Arg Gly Phe Arg Arg Gly Ala Leu Arg Asp Val Arg Asn Arg			
	165	170	175
ttt gaa atc ctg gat agt tta ttt acg caa tat atg cca tct ttt aga			576
Phe Glu Ile Leu Asp Ser Leu Phe Thr Gln Tyr Met Pro Ser Phe Arg			
	180	185	190
gtg aca aat ttt gaa gta cca ttc ctt act gta tat gca atg gca gcc			624
Val Thr Asn Phe Glu Val Pro Phe Leu Thr Val Tyr Ala Met Ala Ala			
	195	200	205
aac ctt cat tta ctg tta tta aag gac gcg tca att ttt gga gaa gaa			672
Asn Leu His Leu Leu Leu Leu Lys Asp Ala Ser Ile Phe Gly Glu Glu			
	210	215	220
tgg gga tgg tca aca act act att aat aac tat tat gat cgt caa atg			720
Trp Gly Trp Ser Thr Thr Thr Ile Asn Asn Tyr Tyr Asp Arg Gln Met			
	225	230	235
aaa ctt act gca gaa tat tct gat cac tgt gta aag tgg tat gaa act			768
Lys Leu Thr Ala Glu Tyr Ser Asp His Cys Val Lys Trp Tyr Glu Thr			
	245	250	255
ggt tta gca aaa tta aaa ggc acg agc gct aaa caa tgg gtt gac tat			816
Gly Leu Ala Lys Leu Lys Gly Thr Ser Ala Lys Gln Trp Val Asp Tyr			
	260	265	270
aac caa ttc cgt aga gaa atg aca ctg gcg gtt tta gat gtt gtt gca			864
Asn Gln Phe Arg Arg Glu Met Thr Leu Ala Val Leu Asp Val Val Ala			
	275	280	285
tta ttc cca aat tat gac aca ata acg tac cca ata gaa acg aaa gca			912
Leu Phe Pro Asn Tyr Asp Thr Ile Thr Tyr Pro Ile Glu Thr Lys Ala			
	290	295	300
caa cta aca agg gaa gta tat aca gat cca ctg ggc gcg gta aac gtg			960
Gln Leu Thr Arg Glu Val Tyr Thr Asp Pro Leu Gly Ala Val Asn Val			
	305	310	315
tct tca att ggt tcc tgg tat gac aaa gca cct tct ttc gga gtg ata			1008
Ser Ser Ile Gly Ser Trp Tyr Asp Lys Ala Pro Ser Phe Gly Val Ile			
	325	330	335
gaa tca tcc gtt att cga cca ccc cat gta ttt gat tat ata acg gga			1056
Glu Ser Ser Val Ile Arg Pro Pro His Val Phe Asp Tyr Ile Thr Gly			
	340	345	350
ctc aca gtg tat aca caa tca aga agc att tct tcc gct cgc tat ata			1104
Leu Thr Val Tyr Thr Gln Ser Arg Ser Ile Ser Ser Ala Arg Tyr Ile			
	355	360	365

aga cat tgg gct ggt cat caa ata agc tac cat cgt gtc agt agg ggt	1152
Arg His Trp Ala Gly His Gln Ile Ser Tyr His Arg Val Ser Arg Gly	
370 375 380	
agt aat ctt caa caa atg tat gga act aat caa aat cta cac agc act	1200
Ser Asn Leu Gln Gln Met Tyr Gly Thr Asn Gln Asn Leu His Ser Thr	
385 390 395 400	
agt acc ttt gat ttt acg aat tat gat att tac aag act cta tca aag	1248
Ser Thr Phe Asp Phe Thr Asn Tyr Asp Ile Tyr Lys Thr Leu Ser Lys	
405 410 415	
gat gca gta ctc ctt gat att gtt tac cct ggt tat acg tat ata ttt	1296
Asp Ala Val Leu Leu Asp Ile Val Tyr Pro Gly Tyr Thr Tyr Ile Phe	
420 425 430	
ttt gga atg cca gaa gtc gag ttt ttc atg gta aac caa ttg aat aat	1344
Phe Gly Met Pro Glu Val Glu Phe Phe Met Val Asn Gln Leu Asn Asn	
435 440 445	
acc aga aag acg tta aag tat aat cca gtt tcc aaa gat att ata gcg	1392
Thr Arg Lys Thr Leu Lys Tyr Asn Pro Val Ser Lys Asp Ile Ile Ala	
450 455 460	
agt aca aga gat tcg gaa tta gaa tta cct cca gaa act tca gat caa	1440
Ser Thr Arg Asp Ser Glu Leu Glu Leu Pro Pro Glu Thr Ser Asp Gln	
465 470 475 480	
cca aat tat gag tca tat agc cat aga tta tgt cat atc aca agt att	1488
Pro Asn Tyr Glu Ser Tyr Ser His Arg Leu Cys His Ile Thr Ser Ile	
485 490 495	
ccc gcg acg ggt aac act acc gga tta gta cct gta ttt tct tgg aca	1536
Pro Ala Thr Gly Asn Thr Thr Gly Leu Val Pro Val Phe Ser Trp Thr	
500 505 510	
cat cga agt gca gat tta aac aat aca ata tat tca gat aaa atc act	1584
His Arg Ser Ala Asp Leu Asn Asn Thr Ile Tyr Ser Asp Lys Ile Thr	
515 520 525	
caa att ccg gcc gtt aaa tgt tgg gat aat tta ccg ttt gtt cca gtg	1632
Gln Ile Pro Ala Val Lys Cys Trp Asp Asn Leu Pro Phe Val Pro Val	
530 535 540	
gta aaa gga cca gga cat aca gga ggg gat tta tta cag tat aat aga	1680
Val Lys Gly Pro Gly His Thr Gly Gly Asp Leu Leu Gln Tyr Asn Arg	
545 550 555 560	
agt act ggt tct gta gga acc tta ttt cta gct cga tat ggc cta gca	1728
Ser Thr Gly Ser Val Gly Thr Leu Phe Leu Ala Arg Tyr Gly Leu Ala	
565 570 575	
tta gaa aaa gca ggg aaa tat cgt gta aga ctg aga tat gct act gat	1776
Leu Glu Lys Ala Gly Lys Tyr Arg Val Arg Leu Arg Tyr Ala Thr Asp	
580 585 590	

gca gat att gta ttg cat gta aac gat gct cag att cag atg cca aaa	1824
Ala Asp Ile Val Leu His Val Asn Asp Ala Gln Ile Gln Met Pro Lys	
595 600 605	
aca atg aac cca ggt gag gat ctg aca tct aaa act ttt aaa gtt gca	1872
Thr Met Asn Pro Gly Glu Asp Leu Thr Ser Lys Thr Phe Lys Val Ala	
610 615 620	
gat gct atc aca aca gtt aat tta gca aca gat agt tcg gtt gca gtt	1920
Asp Ala Ile Thr Thr Val Asn Leu Ala Thr Asp Ser Ser Val Ala Val	
625 630 635 640	
aaa cat aat tta ggt gaa gac cct aat tca aca tta tct ggt ata gtt	1968
Lys His Asn Leu Gly Glu Asp Pro Asn Ser Thr Leu Ser Gly Ile Val	
645 650 655	
tac gtt gac cga atc gaa ttc atc cca gta gat gag aca tat gaa gcg	2016
Tyr Val Asp Arg Ile Glu Phe Ile Pro Val Asp Glu Thr Tyr Glu Ala	
660 665 670	
gaa	2019
Glu	

<210> 88
 <211> 673
 <212> PRT
 <213> Bacillus thuringiensis (mutated)

<400> 88

Met Ser Pro Asn Asn Gln Asn Glu Tyr Glu Ile Ile Asp Ala Thr Pro	
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Ser Thr Ser Val Ser Asn Asp Ser Asn Arg Tyr Pro Phe Ala Asn Glu	
20 25 30	
Pro Thr Asn Ala Leu Gln Asn Met Asp Tyr Lys Asp Tyr Ala Val Gly	
35 40 45	
Ser Ala Gly Asn Ala Ser Glu Tyr Pro Gly Ser Pro Glu Val Leu Val	
50 55 60	
Ser Gly Gln Asp Ala Ala Lys Ala Ala Ile Asp Ile Val Gly Lys Leu	
65 70 75 80	
Leu Ser Gly Leu Gly Val Pro Phe Val Gly Pro Ile Val Ser Leu Tyr	
85 90 95	
Thr Gln Leu Ile Asp Ile Leu Trp Pro Ser Gly Glu Lys Ser Gln Trp	
100 105 110	
Glu Ile Phe Met Glu Gln Val Glu Leu Ile Asn Gln Lys Ile Ala	
115 120 125	
Glu Tyr Ala Arg Asn Lys Ala Leu Ser Glu Leu Glu Gly Leu Gly Asn	
130 135 140	
Asn Tyr Gln Leu Tyr Leu Thr Ala Leu Glu Glu Trp Glu Glu Asn Pro	
145 150 155 160	
Phe Arg Arg Gly Phe Arg Arg Gly Ala Leu Arg Asp Val Arg Asn Arg	
165 170 175	
Phe Glu Ile Leu Asp Ser Leu Phe Thr Gln Tyr Met Pro Ser Phe Arg	
180 185 190	
Val Thr Asn Phe Glu Val Pro Phe Leu Thr Val Tyr Ala Met Ala Ala	
195 200 205	

Asn	Leu	His	Leu	Leu	Leu	Leu	Lys	Asp	Ala	Ser	Ile	Phe	Gly	Glu	Glu
210						215					220				
Trp	Gly	Trp	Ser	Thr	Thr	Thr	Ile	Asn	Asn	Tyr	Tyr	Asp	Arg	Gln	Met
225					230					235					240
Lys	Leu	Thr	Ala	Glu	Tyr	Ser	Asp	His	Cys	Val	Lys	Trp	Tyr	Glu	Thr
				245					250					255	
Gly	Leu	Ala	Lys	Leu	Lys	Gly	Thr	Ser	Ala	Lys	Gln	Trp	Val	Asp	Tyr
			260					265					270		
Asn	Gln	Phe	Arg	Arg	Glu	Met	Thr	Leu	Ala	Val	Leu	Asp	Val	Val	Ala
		275					280					285			
Leu	Phe	Pro	Asn	Tyr	Asp	Thr	Ile	Thr	Tyr	Pro	Ile	Glu	Thr	Lys	Ala
	290					295					300				
Gln	Leu	Thr	Arg	Glu	Val	Tyr	Thr	Asp	Pro	Leu	Gly	Ala	Val	Asn	Val
305					310					315					320
Ser	Ser	Ile	Gly	Ser	Trp	Tyr	Asp	Lys	Ala	Pro	Ser	Phe	Gly	Val	Ile
			325						330					335	
Glu	Ser	Ser	Val	Ile	Arg	Pro	Pro	His	Val	Phe	Asp	Tyr	Ile	Thr	Gly
			340					345					350		
Leu	Thr	Val	Tyr	Thr	Gln	Ser	Arg	Ser	Ile	Ser	Ser	Ala	Arg	Tyr	Ile
	355						360						365		
Arg	His	Trp	Ala	Gly	His	Gln	Ile	Ser	Tyr	His	Arg	Val	Ser	Arg	Gly
	370					375					380				
Ser	Asn	Leu	Gln	Gln	Met	Tyr	Gly	Thr	Asn	Gln	Asn	Leu	His	Ser	Thr
385					390					395					400
Ser	Thr	Phe	Asp	Phe	Thr	Asn	Tyr	Asp	Ile	Tyr	Lys	Thr	Leu	Ser	Lys
			405						410					415	
Asp	Ala	Val	Leu	Leu	Asp	Ile	Val	Tyr	Pro	Gly	Tyr	Thr	Tyr	Ile	Phe
			420					425					430		
Phe	Gly	Met	Pro	Glu	Val	Glu	Phe	Phe	Met	Val	Asn	Gln	Leu	Asn	Asn
	435						440					445			
Thr	Arg	Lys	Thr	Leu	Lys	Tyr	Asn	Pro	Val	Ser	Lys	Asp	Ile	Ile	Ala
	450					455					460				
Ser	Thr	Arg	Asp	Ser	Glu	Leu	Glu	Leu	Pro	Pro	Glu	Thr	Ser	Asp	Gln
465					470					475					480
Pro	Asn	Tyr	Glu	Ser	Tyr	Ser	His	Arg	Leu	Cys	His	Ile	Thr	Ser	Ile
			485						490					495	
Pro	Ala	Thr	Gly	Asn	Thr	Thr	Gly	Leu	Val	Pro	Val	Phe	Ser	Trp	Thr
			500					505					510		
His	Arg	Ser	Ala	Asp	Leu	Asn	Asn	Thr	Ile	Tyr	Ser	Asp	Lys	Ile	Thr
	515						520					525			
Gln	Ile	Pro	Ala	Val	Lys	Cys	Trp	Asp	Asn	Leu	Pro	Phe	Val	Pro	Val
	530					535					540				
Val	Lys	Gly	Pro	Gly	His	Thr	Gly	Gly	Asp	Leu	Leu	Gln	Tyr	Asn	Arg
545					550					555					560
Ser	Thr	Gly	Ser	Val	Gly	Thr	Leu	Phe	Leu	Ala	Arg	Tyr	Gly	Leu	Ala
			565					570						575	
Leu	Glu	Lys	Ala	Gly	Lys	Tyr	Arg	Val	Arg	Leu	Arg	Tyr	Ala	Thr	Asp
			580					585					590		
Ala	Asp	Ile	Val	Leu	His	Val	Asn	Asp	Ala	Gln	Ile	Gln	Met	Pro	Lys
	595						600					605			
Thr	Met	Asn	Pro	Gly	Glu	Asp	Leu	Thr	Ser	Lys	Thr	Phe	Lys	Val	Ala
	610					615						620			
Asp	Ala	Ile	Thr	Thr	Val	Asn	Leu	Ala	Thr	Asp	Ser	Ser	Val	Ala	Val
625					630					635					640
Lys	His	Asn	Leu	Gly	Glu	Asp	Pro	Asn	Ser	Thr	Leu	Ser	Gly	Ile	Val
			645						650					655	
Tyr	Val	Asp	Arg	Ile	Glu	Phe	Ile	Pro	Val	Asp	Glu	Thr	Tyr	Glu	Ala

Glu
 660
665
670

<210> 89
 <211> 2019
 <212> DNA
 <213> *Bacillus thuringiensis* (mutated)

<220>
 <221> CDS
 <222> (1)...(2019)

<400> 89

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tct act tct gta tcc aat gat tct aac aga tac cct ttt gcg aat gag	96
Ser Thr Ser Val Ser Asn Asp Ser Asn Arg Tyr Pro Phe Ala Asn Glu	
20 25 30	
cca aca aat gcg cta caa aat atg gat tat aaa gat tat gca gta ggg	144
Pro Thr Asn Ala Leu Gln Asn Met Asp Tyr Lys Asp Tyr Ala Val Gly	
35 40 45	
tct gcg gga aat gct agt gaa tac cct ggt tca cct gaa gta ctt gtt	192
Ser Ala Gly Asn Ala Ser Glu Tyr Pro Gly Ser Pro Glu Val Leu Val	
50 55 60	
agc gga caa gat gca gct aag gcc gca att gat ata gta ggt aaa tta	240
Ser Gly Gln Asp Ala Ala Lys Ala Ala Ile Asp Ile Val Gly Lys Leu	
65 70 75 80	
cta tca ggt tta ggg gtc cca ttt gtt ggg ccg ata gtg agt ctt tat	288
Leu Ser Gly Leu Gly Val Pro Phe Val Gly Pro Ile Val Ser Leu Tyr	
85 90 95	
act caa ctt att gat att ctg tgg cct tca ggg gaa aag agt caa tgg	336
Thr Gln Leu Ile Asp Ile Leu Trp Pro Ser Gly Glu Lys Ser Gln Trp	
100 105 110	
gaa att ttt atg gaa caa gta gaa gaa ctc att aat caa aaa ata gca	384
Glu Ile Phe Met Glu Gln Val Glu Glu Leu Ile Asn Gln Lys Ile Ala	
115 120 125	
gaa tat gca agg aat aaa gcg ctt tcg gaa tta gaa gga tta ggt aat	432
Glu Tyr Ala Arg Asn Lys Ala Leu Ser Glu Leu Glu Gly Leu Gly Asn	
130 135 140	
aat tac caa tta tat cta act gcg ctt gaa gaa tgg gaa gaa aat cca	480
Asn Tyr Gln Leu Tyr Leu Thr Ala Leu Glu Glu Trp Glu Glu Asn Pro	
145 150 155 160	
ttt cga cga ggt ttt cga cga ggt gcc tta cga gat gtg cga aat cga	528
Phe Arg Arg Gly Phe Arg Arg Gly Ala Leu Arg Asp Val Arg Asn Arg	

165										170					175					
ttt gaa atc ctg gat agt tta ttt acg caa tat atg cca tct ttt aga	576																			
Phe Glu Ile Leu Asp Ser Leu Phe Thr Gln Tyr Met Pro Ser Phe Arg																				
180	185	190																		
gtg aca aat ttt gaa gta cca ttc ctt act gta tat gca atg gca gcc	624																			
Val Thr Asn Phe Glu Val Pro Phe Leu Thr Val Tyr Ala Met Ala Ala																				
195	200	205																		
aac ctt cat tta ctg tta tta aag gac gcg tca att ttt gga gaa gaa	672																			
Asn Leu His Leu Leu Leu Leu Lys Asp Ala Ser Ile Phe Gly Glu Glu																				
210	215	220																		
tgg gga tgg tca aca act act att aat aac tat tat gat cgt caa atg	720																			
Trp Gly Trp Ser Thr Thr Thr Ile Asn Asn Tyr Tyr Asp Arg Gln Met																				
225	230	235	240																	
aaa ctt act gca gaa tat tct gat cac tgt gta aag tgg tat gaa act	768																			
Lys Leu Thr Ala Glu Tyr Ser Asp His Cys Val Lys Trp Tyr Glu Thr																				
245	250	255																		
ggt tta gca aaa tta aaa ggc acg agc gct aaa caa tgg gtt gac tat	816																			
Gly Leu Ala Lys Leu Lys Gly Thr Ser Ala Lys Gln Trp Val Asp Tyr																				
260	265	270																		
aac caa ttc cgt aga gaa atg aca ctg gcg gtt tta gat gtt gtt gca	864																			
Asn Gln Phe Arg Arg Glu Met Thr Leu Ala Val Leu Asp Val Val Ala																				
275	280	285																		
tta ttc cca aat tat gac aca cgt acg tac cca atg gaa acg aaa gca	912																			
Leu Phe Pro Asn Tyr Asp Thr Arg Thr Tyr Pro Met Glu Thr Lys Ala																				
290	295	300																		
caa cta aca agg gaa gta tat aca gat cca ctg ggc gcg gta aac gtg	960																			
Gln Leu Thr Arg Glu Val Tyr Thr Asp Pro Leu Gly Ala Val Asn Val																				
305	310	315	320																	
tct tca att ggt tcc tgg tat gac aaa gca cct tct ttc gga gtg ata	1008																			
Ser Ser Ile Gly Ser Trp Tyr Asp Lys Ala Pro Ser Phe Gly Val Ile																				
325	330	335																		
gaa tca tcc gtt att cga cca ccc cat gta ttt gat tat ata acg gga	1056																			
Glu Ser Ser Val Ile Arg Pro Pro His Val Phe Asp Tyr Ile Thr Gly																				
340	345	350																		
ctc aca gtg tat aca caa tca aga agc att tct tcc gct cgc tat ata	1104																			
Leu Thr Val Tyr Thr Gln Ser Arg Ser Ile Ser Ser Ala Arg Tyr Ile																				
355	360	365																		
aga cat tgg gct ggt cat caa ata agc tac cat cgt gtc agt agg ggt	1152																			
Arg His Trp Ala Gly His Gln Ile Ser Tyr His Arg Val Ser Arg Gly																				
370	375	380																		
agt aat ctt caa caa atg tat gga act aat caa aat cta cac agc act	1200																			
Ser Asn Leu Gln Gln Met Tyr Gly Thr Asn Gln Asn Leu His Ser Thr																				
385	390	395	400																	

agt acc ttt gat ttt acg aat tat gat att tac aag act cta tca aag	1248
Ser Thr Phe Asp Phe Thr Asn Tyr Asp Ile Tyr Lys Thr Leu Ser Lys	
405 410 415	
gat gca gta ctc ctt gat att gtt tac cct ggt tat acg tat ata ttt	1296
Asp Ala Val Leu Leu Asp Ile Val Tyr Pro Gly Tyr Thr Tyr Ile Phe	
420 425 430	
ttt gga atg cca gaa gtc gag ttt ttc atg gta aac caa ttg aat aat	1344
Phe Gly Met Pro Glu Val Glu Phe Phe Met Val Asn Gln Leu Asn Asn	
435 440 445	
acc aga aag acg tta aag tat aat cca gtt tcc aaa gat att ata gcg	1392
Thr Arg Lys Thr Leu Lys Tyr Asn Pro Val Ser Lys Asp Ile Ile Ala	
450 455 460	
agt aca aga gat tcg gaa tta gaa tta cct cca gaa act tca gat caa	1440
Ser Thr Arg Asp Ser Glu Leu Glu Leu Pro Pro Glu Thr Ser Asp Gln	
465 470 475 480	
cca aat tat gag tca tat agc cat aga tta tgt cat atc aca agt att	1488
Pro Asn Tyr Glu Ser Tyr Ser His Arg Leu Cys His Ile Thr Ser Ile	
485 490 495	
ccc gcg acg ggt aac act acc gga tta gta cct gta ttt tct tgg aca	1536
Pro Ala Thr Gly Asn Thr Thr Gly Leu Val Pro Val Phe Ser Trp Thr	
500 505 510	
cat cga agt gca gat tta aac aat aca ata tat tca gat aaa atc act	1584
His Arg Ser Ala Asp Leu Asn Asn Thr Ile Tyr Ser Asp Lys Ile Thr	
515 520 525	
caa att ccg gcc gtt aaa tgt tgg gat aat tta ccg ttt gtt cca gtg	1632
Gln Ile Pro Ala Val Lys Cys Trp Asp Asn Leu Pro Phe Val Pro Val	
530 535 540	
gta aaa gga cca gga cat aca gga ggg gat tta tta cag tat aat aga	1680
Val Lys Gly Pro Gly His Thr Gly Gly Asp Leu Leu Gln Tyr Asn Arg	
545 550 555 560	
agt act ggt tct gta gga acc tta ttt cta gct cga tat ggc cta gca	1728
Ser Thr Gly Ser Val Gly Thr Leu Phe Leu Ala Arg Tyr Gly Leu Ala	
565 570 575	
tta gaa aaa gca ggg aaa tat cgt gta aga ctg aga tat gct act gat	1776
Leu Glu Lys Ala Gly Lys Tyr Arg Val Arg Leu Arg Tyr Ala Thr Asp	
580 585 590	
gca gat att gta ttg cat gta aac gat gct cag att cag atg cca aaa	1824
Ala Asp Ile Val Leu His Val Asn Asp Ala Gln Ile Gln Met Pro Lys	
595 600 605	
aca atg aac cca ggt gag gat ctg aca tct aaa act ttt aaa gtt gca	1872
Thr Met Asn Pro Gly Glu Asp Leu Thr Ser Lys Thr Phe Lys Val Ala	
610 615 620	

gat gct atc aca aca gtt aat tta gca aca gat agt tcg gtt gca gtt	1920
Asp Ala Ile Thr Thr Val Asn Leu Ala Thr Asp Ser Ser Val Ala Val	
625 630 635 640	
aaa cat aat tta ggt gaa gac cct aat tca aca tta tct ggt ata gtt	1968
Lys His Asn Leu Gly Glu Asp Pro Asn Ser Thr Leu Ser Gly Ile Val	
645 650 655	
tac gtt gac cga atc gaa ttc atc cca gta gat gag aca tat gaa gcg	2016
Tyr Val Asp Arg Ile Glu Phe Ile Pro Val Asp Glu Thr Tyr Glu Ala	
660 665 670	
gaa	2019
Glu	

<210> 90
 <211> 673
 <212> PRT
 <213> *Bacillus thuringiensis* (mutated)

<400> 90

Met Ser Pro Asn Asn Gln Asn Glu Tyr Glu Ile Ile Asp Ala Thr Pro	
1 5 10 15	
Ser Thr Ser Val Ser Asn Asp Ser Asn Arg Tyr Pro Phe Ala Asn Glu	
20 25 30	
Pro Thr Asn Ala Leu Gln Asn Met Asp Tyr Lys Asp Tyr Ala Val Gly	
35 40 45	
Ser Ala Gly Asn Ala Ser Glu Tyr Pro Gly Ser Pro Glu Val Leu Val	
50 55 60	
Ser Gly Gln Asp Ala Ala Lys Ala Ala Ile Asp Ile Val Gly Lys Leu	
65 70 75 80	
Leu Ser Gly Leu Gly Val Pro Phe Val Gly Pro Ile Val Ser Leu Tyr	
85 90 95	
Thr Gln Leu Ile Asp Ile Leu Trp Pro Ser Gly Glu Lys Ser Gln Trp	
100 105 110	
Glu Ile Phe Met Glu Gln Val Glu Glu Leu Ile Asn Gln Lys Ile Ala	
115 120 125	
Glu Tyr Ala Arg Asn Lys Ala Leu Ser Glu Leu Glu Gly Leu Gly Asn	
130 135 140	
Asn Tyr Gln Leu Tyr Leu Thr Ala Leu Glu Glu Trp Glu Glu Asn Pro	
145 150 155 160	
Phe Arg Arg Gly Phe Arg Arg Gly Ala Leu Arg Asp Val Arg Asn Arg	
165 170 175	
Phe Glu Ile Leu Asp Ser Leu Phe Thr Gln Tyr Met Pro Ser Phe Arg	
180 185 190	
Val Thr Asn Phe Glu Val Pro Phe Leu Thr Val Tyr Ala Met Ala Ala	
195 200 205	
Asn Leu His Leu Leu Leu Lys Asp Ala Ser Ile Phe Gly Glu Glu	
210 215 220	
Trp Gly Trp Ser Thr Thr Thr Ile Asn Asn Tyr Tyr Asp Arg Gln Met	
225 230 235 240	
Lys Leu Thr Ala Glu Tyr Ser Asp His Cys Val Lys Trp Tyr Glu Thr	
245 250 255	
Gly Leu Ala Lys Leu Lys Gly Thr Ser Ala Lys Gln Trp Val Asp Tyr	
260 265 270	

Asn	Gln	Phe	Arg	Arg	Glu	Met	Thr	Leu	Ala	Val	Leu	Asp	Val	Val	Ala	
		275					280					285				
Leu	Phe	Pro	Asn	Tyr	Asp	Thr	Arg	Thr	Tyr	Pro	Met	Glu	Thr	Lys	Ala	
		290				295					300					
Gln	Leu	Thr	Arg	Glu	Val	Tyr	Thr	Asp	Pro	Leu	Gly	Ala	Val	Asn	Val	
305					310						315				320	
Ser	Ser	Ile	Gly	Ser	Trp	Tyr	Asp	Lys	Ala	Pro	Ser	Phe	Gly	Val	Ile	
				325					330					335		
Glu	Ser	Ser	Val	Ile	Arg	Pro	Pro	His	Val	Phe	Asp	Tyr	Ile	Thr	Gly	
			340					345					350			
Leu	Thr	Val	Tyr	Thr	Gln	Ser	Arg	Ser	Ile	Ser	Ser	Ala	Arg	Tyr	Ile	
		355					360					365				
Arg	His	Trp	Ala	Gly	His	Gln	Ile	Ser	Tyr	His	Arg	Val	Ser	Arg	Gly	
		370				375					380					
Ser	Asn	Leu	Gln	Gln	Met	Tyr	Gly	Thr	Asn	Gln	Asn	Leu	His	Ser	Thr	
385					390					395					400	
Ser	Thr	Phe	Asp	Phe	Thr	Asn	Tyr	Asp	Ile	Tyr	Lys	Thr	Leu	Ser	Lys	
				405					410					415		
Asp	Ala	Val	Leu	Leu	Asp	Ile	Val	Tyr	Pro	Gly	Tyr	Thr	Tyr	Ile	Phe	
			420					425					430			
Phe	Gly	Met	Pro	Glu	Val	Glu	Phe	Phe	Met	Val	Asn	Gln	Leu	Asn	Asn	
		435					440					445				
Thr	Arg	Lys	Thr	Leu	Lys	Tyr	Asn	Pro	Val	Ser	Lys	Asp	Ile	Ile	Ala	
		450				455					460					
Ser	Thr	Arg	Asp	Ser	Glu	Leu	Glu	Leu	Pro	Pro	Glu	Thr	Ser	Asp	Gln	
465					470					475					480	
Pro	Asn	Tyr	Glu	Ser	Tyr	Ser	His	Arg	Leu	Cys	His	Ile	Thr	Ser	Ile	
				485					490					495		
Pro	Ala	Thr	Gly	Asn	Thr	Thr	Gly	Leu	Val	Pro	Val	Phe	Ser	Trp	Thr	
		500					505						510			
His	Arg	Ser	Ala	Asp	Leu	Asn	Asn	Thr	Ile	Tyr	Ser	Asp	Lys	Ile	Thr	
		515					520					525				
Gln	Ile	Pro	Ala	Val	Lys	Cys	Trp	Asp	Asn	Leu	Pro	Phe	Val	Pro	Val	
		530				535					540					
Val	Lys	Gly	Pro	Gly	His	Thr	Gly	Gly	Asp	Leu	Leu	Gln	Tyr	Asn	Arg	
545					550					555					560	
Ser	Thr	Gly	Ser	Val	Gly	Thr	Leu	Phe	Leu	Ala	Arg	Tyr	Gly	Leu	Ala	
				565					570					575		
Leu	Glu	Lys	Ala	Gly	Lys	Tyr	Arg	Val	Arg	Leu	Arg	Tyr	Ala	Thr	Asp	
			580					585					590			
Ala	Asp	Ile	Val	Leu	His	Val	Asn	Asp	Ala	Gln	Ile	Gln	Met	Pro	Lys	
		595					600					605				
Thr	Met	Asn	Pro	Gly	Glu	Asp	Leu	Thr	Ser	Lys	Thr	Phe	Lys	Val	Ala	
		610				615					620					
Asp	Ala	Ile	Thr	Thr	Val	Asn	Leu	Ala	Thr	Asp	Ser	Ser	Val	Ala	Val	
625					630					635					640	
Lys	His	Asn	Leu	Gly	Glu	Asp	Pro	Asn	Ser	Thr	Leu	Ser	Gly	Ile	Val	
				645					650					655		
Tyr	Val	Asp	Arg	Ile	Glu	Phe	Ile	Pro	Val	Asp	Glu	Thr	Tyr	Glu	Ala	
			660					665					670			

Glu

<210> 91
 <211> 2019
 <212> DNA

<213> *Bacillus thuringiensis* (mutated)

<220>

<221> CDS

<222> (1)...(2019)

<400> 91

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Met Ser Pro Asn Asn Gln Asn Glu Tyr Glu Ile Ile Asp Ala Thr Pro	
1 5 10 15	
tct act tct gta tcc aat gat tct aac aga tac cct ttt gcg aat gag	96
Ser Thr Ser Val Ser Asn Asp Ser Asn Arg Tyr Pro Phe Ala Asn Glu	
20 25 30	
cca aca aat gcg cta caa aat atg gat tat aaa gat tat tta aaa atg	144
Pro Thr Asn Ala Leu Gln Asn Met Asp Tyr Lys Asp Tyr Leu Lys Met	
35 40 45	
tct gcg gga aat gct agt gaa tac cct ggt tca cct gaa gta ctt gtt	192
Ser Ala Gly Asn Ala Ser Glu Tyr Pro Gly Ser Pro Glu Val Leu Val	
50 55 60	
agc gga caa gat gca gct aag gcc gca att gat ata gta ggt aaa tta	240
Ser Gly Gln Asp Ala Ala Lys Ala Ala Ile Asp Ile Val Gly Lys Leu	
65 70 75 80	
cta tca ggt tta ggg gtc cca ttt gtt ggg ccg ata gtg agt ctt tat	288
Leu Ser Gly Leu Gly Val Pro Phe Val Gly Pro Ile Val Ser Leu Tyr	
85 90 95	
act caa ctt att gat att ctg tgg cct tca ggg gaa aag agt caa tgg	336
Thr Gln Leu Ile Asp Ile Leu Trp Pro Ser Gly Glu Lys Ser Gln Trp	
100 105 110	
gaa att ttt atg gaa caa gta gaa gaa ctc att aat caa aaa ata gca	384
Glu Ile Phe Met Glu Gln Val Glu Glu Leu Ile Asn Gln Lys Ile Ala	
115 120 125	
gaa tat gca agg aat aaa gcg ctt tcg gaa tta gaa gga tta ggt aat	432
Glu Tyr Ala Arg Asn Lys Ala Leu Ser Glu Leu Glu Gly Leu Gly Asn	
130 135 140	
aat tac caa tta tat cta act gcg ctt gaa gaa tgg gaa gaa aat cca	480
Asn Tyr Gln Leu Tyr Leu Thr Ala Leu Glu Glu Trp Glu Glu Asn Pro	
145 150 155 160	
ttt cga cga ggt ttt cga cga ggt gcc tta cga gat gtg cga aat cga	528
Phe Arg Arg Gly Phe Arg Arg Gly Ala Leu Arg Asp Val Arg Asn Arg	
165 170 175	
ttt gaa atc ctg gat agt tta ttt acg caa tat atg cca tct ttt aga	576
Phe Glu Ile Leu Asp Ser Leu Phe Thr Gln Tyr Met Pro Ser Phe Arg	
180 185 190	
gtg aca aat ttt gaa gta cca ttc ctt act gta tat gca atg gca gcc	624
Val Thr Asn Phe Glu Val Pro Phe Leu Thr Val Tyr Ala Met Ala Ala	

195	200	205	
aac ctt cat tta ctg tta tta aag gac gcg tca att ttt gga gaa gaa			672
Asn Leu His Leu Leu Leu Lys Asp Ala Ser Ile Phe Gly Glu Glu			
210	215	220	
tgg gga tgg tca aca act act att aat aac tat tat gat cgt caa atg			720
Trp Gly Trp Ser Thr Thr Thr Ile Asn Asn Tyr Tyr Asp Arg Gln Met			
225	230	235	240
aaa ctt act gca gaa tat tct gat cac tgt gta aag tgg tat gaa act			768
Lys Leu Thr Ala Glu Tyr Ser Asp His Cys Val Lys Trp Tyr Glu Thr			
245	250	255	
ggg tta gca aaa tta aaa ggc acg agc gct aaa caa tgg gtt gac tat			816
Gly Leu Ala Lys Leu Lys Gly Thr Ser Ala Lys Gln Trp Val Asp Tyr			
260	265	270	
aac caa ttc cgt aga gaa atg aca ctg gcg gtt tta gat gtt gtt gca			864
Asn Gln Phe Arg Arg Glu Met Thr Leu Ala Val Leu Asp Val Val Ala			
275	280	285	
tta ttc cca aat tat gac aca ata acg tac cca atg gaa acg aaa gca			912
Leu Phe Pro Asn Tyr Asp Thr Ile Thr Tyr Pro Met Glu Thr Lys Ala			
290	295	300	
caa cta aca agg gaa gta tat aca gat cca ctg ggc gcg gta aac gtg			960
Gln Leu Thr Arg Glu Val Tyr Thr Asp Pro Leu Gly Ala Val Asn Val			
305	310	315	320
tct tca att ggt tcc tgg tat gac aaa gca cct tct ttc gga gtg ata			1008
Ser Ser Ile Gly Ser Trp Tyr Asp Lys Ala Pro Ser Phe Gly Val Ile			
325	330	335	
gaa tca tcc gtt att cga cca ccc cat gta ttt gat tat ata acg gga			1056
Glu Ser Ser Val Ile Arg Pro Pro His Val Phe Asp Tyr Ile Thr Gly			
340	345	350	
ctc aca gtg tat aca caa tca aga agc att tct tcc gct cgc tat ata			1104
Leu Thr Val Tyr Thr Gln Ser Arg Ser Ile Ser Ser Ala Arg Tyr Ile			
355	360	365	
aga cat tgg gct ggt cat caa ata agc tac cat cgt gtc agt agg ggt			1152
Arg His Trp Ala Gly His Gln Ile Ser Tyr His Arg Val Ser Arg Gly			
370	375	380	
agt aat ctt caa caa atg tat gga act aat caa aat cta cac agc act			1200
Ser Asn Leu Gln Gln Met Tyr Gly Thr Asn Gln Asn Leu His Ser Thr			
385	390	395	400
agt acc ttt gat ttt acg aat tat gat att tac aag act cta tca aag			1248
Ser Thr Phe Asp Phe Thr Asn Tyr Asp Ile Tyr Lys Thr Leu Ser Lys			
405	410	415	
gat gca gta ctc ctt gat att gtt tac cct ggt tat acg tat ata ttt			1296
Asp Ala Val Leu Leu Asp Ile Val Tyr Pro Gly Tyr Thr Tyr Ile Phe			
420	425	430	

ttt gga atg cca gaa gtc gag ttt ttc atg gta aac caa ttg aat aat	1344
Phe Gly Met Pro Glu Val Glu Phe Phe Met Val Asn Gln Leu Asn Asn	
435 440 445	
acc aga aag acg tta aag tat aat cca gtt tcc aaa gat att ata gcg	1392
Thr Arg Lys Thr Leu Lys Tyr Asn Pro Val Ser Lys Asp Ile Ile Ala	
450 455 460	
agt aca aga gat tcg gaa tta gaa tta cct cca gaa act tca gat caa	1440
Ser Thr Arg Asp Ser Glu Leu Glu Leu Pro Pro Glu Thr Ser Asp Gln	
465 470 475 480	
cca aat tat gag tca tat agc cat aga tta tgt cat atc aca agt att	1488
Pro Asn Tyr Glu Ser Tyr Ser His Arg Leu Cys His Ile Thr Ser Ile	
485 490 495	
ccc gcg acg ggt aac act acc gga tta gta cct gta ttt tct tgg aca	1536
Pro Ala Thr Gly Asn Thr Thr Gly Leu Val Pro Val Phe Ser Trp Thr	
500 505 510	
cat cga agt gca gat tta aac aat aca ata tat tca gat aaa atc act	1584
His Arg Ser Ala Asp Leu Asn Asn Thr Ile Tyr Ser Asp Lys Ile Thr	
515 520 525	
caa att ccg gcc gtt aaa tgt tgg gat aat tta ccg ttt gtt cca gtg	1632
Gln Ile Pro Ala Val Lys Cys Trp Asp Asn Leu Pro Phe Val Pro Val	
530 535 540	
gta aaa gga cca gga cat aca gga ggg gat tta tta cag tat aat aga	1680
Val Lys Gly Pro Gly His Thr Gly Gly Asp Leu Leu Gln Tyr Asn Arg	
545 550 555 560	
agt act ggt tct gta gga acc tta ttt cta gct cga tat ggc cta gca	1728
Ser Thr Gly Ser Val Gly Thr Leu Phe Leu Ala Arg Tyr Gly Leu Ala	
565 570 575	
tta gaa aaa gca ggg aaa tat cgt gta aga ctg aga tat gct act gat	1776
Leu Glu Lys Ala Gly Lys Tyr Arg Val Arg Leu Arg Tyr Ala Thr Asp	
580 585 590	
gca gat att gta ttg cat gta aac gat gct cag att cag atg cca aaa	1824
Ala Asp Ile Val Leu His Val Asn Asp Ala Gln Ile Gln Met Pro Lys	
595 600 605	
aca atg aac cca ggt gag gat ctg aca tct aaa act ttt aaa gtt gca	1872
Thr Met Asn Pro Gly Glu Asp Leu Thr Ser Lys Thr Phe Lys Val Ala	
610 615 620	
gat gct atc aca aca gtt aat tta gca aca gat agt tcg gtt gca gtt	1920
Asp Ala Ile Thr Thr Val Asn Leu Ala Thr Asp Ser Ser Val Ala Val	
625 630 635 640	
aaa cat aat tta ggt gaa gac cct aat tca aca tta tct ggt ata gtt	1968
Lys His Asn Leu Gly Glu Asp Pro Asn Ser Thr Leu Ser Gly Ile Val	
645 650 655	

tac gtt gac cga atc gaa ttc atc cca gta gat gag aca tat gaa gcg 2016
 Tyr Val Asp Arg Ile Glu Phe Ile Pro Val Asp Glu Thr Tyr Glu Ala
 660 670

gaa 2019
 Glu

<210> 92
 <211> 673
 <212> PRT
 <213> Bacillus thuringiensis (mutated)

<400> 92
 Met Ser Pro Asn Asn Gln Asn Glu Tyr Glu Ile Ile Asp Ala Thr Pro
 1 5 10 15
 Ser Thr Ser Val Ser Asn Asp Ser Asn Arg Tyr Pro Phe Ala Asn Glu
 20 25 30
 Pro Thr Asn Ala Leu Gln Asn Met Asp Tyr Lys Asp Tyr Leu Lys Met
 35 40 45
 Ser Ala Gly Asn Ala Ser Glu Tyr Pro Gly Ser Pro Glu Val Leu Val
 50 55 60
 Ser Gly Gln Asp Ala Ala Lys Ala Ala Ile Asp Ile Val Gly Lys Leu
 65 70 75 80
 Leu Ser Gly Leu Gly Val Pro Phe Val Gly Pro Ile Val Ser Leu Tyr
 85 90 95
 Thr Gln Leu Ile Asp Ile Leu Trp Pro Ser Gly Glu Lys Ser Gln Trp
 100 105 110
 Glu Ile Phe Met Glu Gln Val Glu Glu Leu Ile Asn Gln Lys Ile Ala
 115 120 125
 Glu Tyr Ala Arg Asn Lys Ala Leu Ser Glu Leu Glu Gly Leu Gly Asn
 130 135 140
 Asn Tyr Gln Leu Tyr Leu Thr Ala Leu Glu Glu Trp Glu Glu Asn Pro
 145 150 155 160
 Phe Arg Arg Gly Phe Arg Arg Gly Ala Leu Arg Asp Val Arg Asn Arg
 165 170 175
 Phe Glu Ile Leu Asp Ser Leu Phe Thr Gln Tyr Met Pro Ser Phe Arg
 180 185 190
 Val Thr Asn Phe Glu Val Pro Phe Leu Thr Val Tyr Ala Met Ala Ala
 195 200 205
 Asn Leu His Leu Leu Leu Leu Lys Asp Ala Ser Ile Phe Gly Glu Glu
 210 215 220
 Trp Gly Trp Ser Thr Thr Thr Ile Asn Asn Tyr Tyr Asp Arg Gln Met
 225 230 235 240
 Lys Leu Thr Ala Glu Tyr Ser Asp His Cys Val Lys Trp Tyr Glu Thr
 245 250 255
 Gly Leu Ala Lys Leu Lys Gly Thr Ser Ala Lys Gln Trp Val Asp Tyr
 260 265 270
 Asn Gln Phe Arg Arg Glu Met Thr Leu Ala Val Leu Asp Val Val Ala
 275 280 285
 Leu Phe Pro Asn Tyr Asp Thr Ile Thr Tyr Pro Met Glu Thr Lys Ala
 290 295 300
 Gln Leu Thr Arg Glu Val Tyr Thr Asp Pro Leu Gly Ala Val Asn Val
 305 310 315 320
 Ser Ser Ile Gly Ser Trp Tyr Asp Lys Ala Pro Ser Phe Gly Val Ile
 325 330 335

Glu Ser Ser Val Ile Arg Pro Pro His Val Phe Asp Tyr Ile Thr Gly
 340 345 350
 Leu Thr Val Tyr Thr Gln Ser Arg Ser Ile Ser Ser Ala Arg Tyr Ile
 355 360 365
 Arg His Trp Ala Gly His Gln Ile Ser Tyr His Arg Val Ser Arg Gly
 370 375 380
 Ser Asn Leu Gln Gln Met Tyr Gly Thr Asn Gln Asn Leu His Ser Thr
 385 390 395 400
 Ser Thr Phe Asp Phe Thr Asn Tyr Asp Ile Tyr Lys Thr Leu Ser Lys
 405 410 415
 Asp Ala Val Leu Leu Asp Ile Val Tyr Pro Gly Tyr Thr Tyr Ile Phe
 420 425 430
 Phe Gly Met Pro Glu Val Glu Phe Phe Met Val Asn Gln Leu Asn Asn
 435 440 445
 Thr Arg Lys Thr Leu Lys Tyr Asn Pro Val Ser Lys Asp Ile Ile Ala
 450 455 460
 Ser Thr Arg Asp Ser Glu Leu Glu Leu Pro Pro Glu Thr Ser Asp Gln
 465 470 475 480
 Pro Asn Tyr Glu Ser Tyr Ser His Arg Leu Cys His Ile Thr Ser Ile
 485 490 495
 Pro Ala Thr Gly Asn Thr Thr Gly Leu Val Pro Val Phe Ser Trp Thr
 500 505 510
 His Arg Ser Ala Asp Leu Asn Asn Thr Ile Tyr Ser Asp Lys Ile Thr
 515 520 525
 Gln Ile Pro Ala Val Lys Cys Trp Asp Asn Leu Pro Phe Val Pro Val
 530 535 540
 Val Lys Gly Pro Gly His Thr Gly Gly Asp Leu Leu Gln Tyr Asn Arg
 545 550 555 560
 Ser Thr Gly Ser Val Gly Thr Leu Phe Leu Ala Arg Tyr Gly Leu Ala
 565 570 575
 Leu Glu Lys Ala Gly Lys Tyr Arg Val Arg Leu Arg Tyr Ala Thr Asp
 580 585 590
 Ala Asp Ile Val Leu His Val Asn Asp Ala Gln Ile Gln Met Pro Lys
 595 600 605
 Thr Met Asn Pro Gly Glu Asp Leu Thr Ser Lys Thr Phe Lys Val Ala
 610 615 620
 Asp Ala Ile Thr Thr Val Asn Leu Ala Thr Asp Ser Ser Val Ala Val
 625 630 635 640
 Lys His Asn Leu Gly Glu Asp Pro Asn Ser Thr Leu Ser Gly Ile Val
 645 650 655
 Tyr Val Asp Arg Ile Glu Phe Ile Pro Val Asp Glu Thr Tyr Glu Ala
 660 665 670
 Glu

<210> 93

<211> 2019

<212> DNA

<213> *Bacillus thuringiensis* (mutated)

<220>

<221> CDS

<222> (1)...(2019)

<400> 93

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Met	Ser	Pro	Asn	Asn	Gln	Asn	Glu	Tyr	Glu	Ile	Ile	Asp	Ala	Thr	Pro	
1				5					10					15		
tct	act	tct	gta	tcc	aat	gat	tct	aac	aga	tac	cct	ttt	gcg	aat	gag	96
Ser	Thr	Ser	Val	Ser	Asn	Asp	Ser	Asn	Arg	Tyr	Pro	Phe	Ala	Asn	Glu	
			20					25					30			
cca	aca	aat	gcg	cta	caa	aat	atg	gat	tat	aaa	gat	tat	tta	aaa	atg	144
Pro	Thr	Asn	Ala	Leu	Gln	Asn	Met	Asp	Tyr	Lys	Asp	Tyr	Leu	Lys	Met	
		35					40					45				
tct	gcg	gga	aat	gct	agt	gaa	tac	cct	ggg	tca	cct	gaa	gta	ctt	gtt	192
Ser	Ala	Gly	Asn	Ala	Ser	Glu	Tyr	Pro	Gly	Ser	Pro	Glu	Val	Leu	Val	
	50					55					60					
agc	gga	caa	gat	gca	gct	aag	gcc	gca	att	gat	ata	gta	ggg	aaa	tta	240
Ser	Gly	Gln	Asp	Ala	Ala	Lys	Ala	Ala	Ile	Asp	Ile	Val	Gly	Lys	Leu	
65					70					75					80	
cta	tca	ggg	tta	ggg	gtc	cca	ttt	gtt	ggg	ccg	ata	gtg	agt	ctt	tat	288
Leu	Ser	Gly	Leu	Gly	Val	Pro	Phe	Val	Gly	Pro	Ile	Val	Ser	Leu	Tyr	
			85					90						95		
act	caa	ctt	att	gat	att	ctg	tgg	cct	tca	ggg	gaa	aag	agt	caa	tgg	336
Thr	Gln	Leu	Ile	Asp	Ile	Leu	Trp	Pro	Ser	Gly	Glu	Lys	Ser	Gln	Trp	
		100						105					110			
gaa	att	ttt	atg	gaa	caa	gta	gaa	gaa	ctc	att	aat	caa	aaa	ata	gca	384
Glu	Ile	Phe	Met	Glu	Gln	Val	Glu	Glu	Leu	Ile	Asn	Gln	Lys	Ile	Ala	
		115					120					125				
gaa	tat	gca	agg	aat	aaa	gcg	ctt	tcg	gaa	tta	gaa	gga	tta	ggg	aat	432
Glu	Tyr	Ala	Arg	Asn	Lys	Ala	Leu	Ser	Glu	Leu	Glu	Gly	Leu	Gly	Asn	
	130					135					140					
aat	tac	caa	tta	tat	cta	act	gcg	ctt	gaa	gaa	tgg	gaa	gaa	aat	cca	480
Asn	Tyr	Gln	Leu	Tyr	Leu	Thr	Ala	Leu	Glu	Glu	Trp	Glu	Glu	Asn	Pro	
145					150					155					160	
ttt	cga	cga	ggg	ttt	cga	cga	ggg	gcc	tta	cga	gat	gtg	cga	aat	cga	528
Phe	Arg	Arg	Gly	Phe	Arg	Arg	Gly	Ala	Leu	Arg	Asp	Val	Arg	Asn	Arg	
			165					170						175		
ttt	gaa	atc	ctg	gat	agt	tta	ttt	acg	caa	tat	atg	cca	tct	ttt	aga	576
Phe	Glu	Ile	Leu	Asp	Ser	Leu	Phe	Thr	Gln	Tyr	Met	Pro	Ser	Phe	Arg	
		180						185					190			
gtg	aca	aat	ttt	gaa	gta	cca	ttc	ctt	act	gta	tat	gca	atg	gca	gcc	624
Val	Thr	Asn	Phe	Glu	Val	Pro	Phe	Leu	Thr	Val	Tyr	Ala	Met	Ala	Ala	
		195					200					205				
aac	ctt	cat	tta	ctg	tta	tta	aag	gac	gcg	tca	att	ttt	gga	gaa	gaa	672
Asn	Leu	His	Leu	Leu	Leu	Leu	Lys	Asp	Ala	Ser	Ile	Phe	Gly	Glu	Glu	
	210					215					220					
tgg	gga	tgg	tca	aca	act	act	att	aat	aac	gtg	gtg	gat	cgt	caa	atg	720
Trp	Gly	Trp	Ser	Thr	Thr	Thr	Ile	Asn	Asn	Val	Val	Asp	Arg	Gln	Met	

225	230	235	240	
aaa ctt act gca gaa tat tct gat cac tgt gta aag tgg tat gaa act				768
Lys Leu Thr Ala Glu Tyr Ser Asp His Cys Val Lys Trp Tyr Glu Thr				
	245	250	255	
ggc tta gca aaa tta aaa ggc acg agc gct aaa caa tgg gtt gac tat				816
Gly Leu Ala Lys Leu Lys Gly Thr Ser Ala Lys Gln Trp Val Asp Tyr				
	260	265	270	
aac caa ttc cgt aga gaa atg aca ctg gcg gtt tta gat gtt gtt gca				864
Asn Gln Phe Arg Arg Glu Met Thr Leu Ala Val Leu Asp Val Val Ala				
	275	280	285	
tta ttc cca aat tat gac aca ata acg tac cca ata gaa acg aaa gca				912
Leu Phe Pro Asn Tyr Asp Thr Ile Thr Tyr Pro Ile Glu Thr Lys Ala				
	290	295	300	
caa cta aca agg gaa gta tat aca gat cca ctg ggc gcg gta aac gtg				960
Gln Leu Thr Arg Glu Val Tyr Thr Asp Pro Leu Gly Ala Val Asn Val				
	305	310	315	320
tct tca att ggt tcc tgg tat gac aaa gca cct tct ttc gga gtg ata				1008
Ser Ser Ile Gly Ser Trp Tyr Asp Lys Ala Pro Ser Phe Gly Val Ile				
	325	330	335	
gaa tca tcc gtt att cga cca ccc cat gta ttt gat tat ata acg gga				1056
Glu Ser Ser Val Ile Arg Pro Pro His Val Phe Asp Tyr Ile Thr Gly				
	340	345	350	
ctc aca gtg tat aca caa tca aga agc att tct tcc gct cgc tat ata				1104
Leu Thr Val Tyr Thr Gln Ser Arg Ser Ile Ser Ser Ala Arg Tyr Ile				
	355	360	365	
aga cat tgg gct ggt cat caa ata agc tac cat cgt gtc agt agg ggt				1152
Arg His Trp Ala Gly His Gln Ile Ser Tyr His Arg Val Ser Arg Gly				
	370	375	380	
agt aat ctt caa caa atg tat gga act aat caa aat cta cac agc act				1200
Ser Asn Leu Gln Gln Met Tyr Gly Thr Asn Gln Asn Leu His Ser Thr				
	385	390	395	400
agt acc ttt gat ttt acg aat tat gat att tac aag act cta tca aag				1248
Ser Thr Phe Asp Phe Thr Asn Tyr Asp Ile Tyr Lys Thr Leu Ser Lys				
	405	410	415	
gat gca gta ctc ctt gat att gtt tac cct ggt tat acg tat ata ttt				1296
Asp Ala Val Leu Leu Asp Ile Val Tyr Pro Gly Tyr Thr Tyr Ile Phe				
	420	425	430	
ttt gga atg cca gaa gtc gag ttt ttc atg gta aac caa ttg aat aat				1344
Phe Gly Met Pro Glu Val Glu Phe Phe Met Val Asn Gln Leu Asn Asn				
	435	440	445	
acc aga aag acg tta aag tat aat cca gtt tcc aaa gat att ata gcg				1392
Thr Arg Lys Thr Leu Lys Tyr Asn Pro Val Ser Lys Asp Ile Ile Ala				
	450	455	460	

agt aca aga gat tcg gaa tta gaa tta cct cca gaa act tca gat caa	1440
Ser Thr Arg Asp Ser Glu Leu Glu Leu Pro Pro Glu Thr Ser Asp Gln	
465 470 475 480	
cca aat tat gag tca tat agc cat aga tta tgt cat atc aca agt att	1488
Pro Asn Tyr Glu Ser Tyr Ser His Arg Leu Cys His Ile Thr Ser Ile	
485 490 495	
ccc gcg acg ggt aac act acc gga tta gta cct gta ttt tct tgg aca	1536
Pro Ala Thr Gly Asn Thr Thr Gly Leu Val Pro Val Phe Ser Trp Thr	
500 505 510	
cat cga agt gca gat tta aac aat aca ata tat tca gat aaa atc act	1584
His Arg Ser Ala Asp Leu Asn Asn Thr Ile Tyr Ser Asp Lys Ile Thr	
515 520 525	
caa att ccg gcc gtt aaa tgt tgg gat aat tta ccg ttt gtt cca gtg	1632
Gln Ile Pro Ala Val Lys Cys Trp Asp Asn Leu Pro Phe Val Pro Val	
530 535 540	
gta aaa gga cca gga cat aca gga ggg gat tta tta cag tat aat aga	1680
Val Lys Gly Pro Gly His Thr Gly Gly Asp Leu Leu Gln Tyr Asn Arg	
545 550 555 560	
agt act ggt tct gta gga acc tta ttt cta gct cga tat ggc cta gca	1728
Ser Thr Gly Ser Val Gly Thr Leu Phe Leu Ala Arg Tyr Gly Leu Ala	
565 570 575	
tta gaa aaa gca ggg aaa tat cgt gta aga ctg aga tat gct act gat	1776
Leu Glu Lys Ala Gly Lys Tyr Arg Val Arg Leu Arg Tyr Ala Thr Asp	
580 585 590	
gca gat att gta ttg cat gta aac gat gct cag att cag atg cca aaa	1824
Ala Asp Ile Val Leu His Val Asn Asp Ala Gln Ile Gln Met Pro Lys	
595 600 605	
aca atg aac cca ggt gag gat ctg aca tct aaa act ttt aaa gtt gca	1872
Thr Met Asn Pro Gly Glu Asp Leu Thr Ser Lys Thr Phe Lys Val Ala	
610 615 620	
gat gct atc aca aca gtt aat tta gca aca gat agt tcg gtt gca gtt	1920
Asp Ala Ile Thr Thr Val Asn Leu Ala Thr Asp Ser Ser Val Ala Val	
625 630 635 640	
aaa cat aat tta ggt gaa gac cct aat tca aca tta tct ggt ata gtt	1968
Lys His Asn Leu Gly Glu Asp Pro Asn Ser Thr Leu Ser Gly Ile Val	
645 650 655	
tac gtt gac cga atc gaa ttc atc cca gta gat gag aca tat gaa gcg	2016
Tyr Val Asp Arg Ile Glu Phe Ile Pro Val Asp Glu Thr Tyr Glu Ala	
660 665 670	
gaa	2019
Glu	

<210> 94
 <211> 673
 <212> PRT
 <213> *Bacillus thuringiensis* (mutated)

<400> 94
 Met Ser Pro Asn Asn Gln Asn Glu Tyr Glu Ile Ile Asp Ala Thr Pro
 1 5 10 15
 Ser Thr Ser Val Ser Asn Asp Ser Asn Arg Tyr Pro Phe Ala Asn Glu
 20 25 30
 Pro Thr Asn Ala Leu Gln Asn Met Asp Tyr Lys Asp Tyr Leu Lys Met
 35 40 45
 Ser Ala Gly Asn Ala Ser Glu Tyr Pro Gly Ser Pro Glu Val Leu Val
 50 55 60
 Ser Gly Gln Asp Ala Ala Lys Ala Ala Ile Asp Ile Val Gly Lys Leu
 65 70 75 80
 Leu Ser Gly Leu Gly Val Pro Phe Val Gly Pro Ile Val Ser Leu Tyr
 85 90 95
 Thr Gln Leu Ile Asp Ile Leu Trp Pro Ser Gly Glu Lys Ser Gln Trp
 100 105 110
 Glu Ile Phe Met Glu Gln Val Glu Glu Leu Ile Asn Gln Lys Ile Ala
 115 120 125
 Glu Tyr Ala Arg Asn Lys Ala Leu Ser Glu Leu Glu Gly Leu Gly Asn
 130 135 140
 Asn Tyr Gln Leu Tyr Leu Thr Ala Leu Glu Glu Trp Glu Glu Asn Pro
 145 150 155 160
 Phe Arg Arg Gly Phe Arg Arg Gly Ala Leu Arg Asp Val Arg Asn Arg
 165 170 175
 Phe Glu Ile Leu Asp Ser Leu Phe Thr Gln Tyr Met Pro Ser Phe Arg
 180 185 190
 Val Thr Asn Phe Glu Val Pro Phe Leu Thr Val Tyr Ala Met Ala Ala
 195 200 205
 Asn Leu His Leu Leu Leu Leu Lys Asp Ala Ser Ile Phe Gly Glu Glu
 210 215 220
 Trp Gly Trp Ser Thr Thr Thr Ile Asn Asn Val Val Asp Arg Gln Met
 225 230 235 240
 Lys Leu Thr Ala Glu Tyr Ser Asp His Cys Val Lys Trp Tyr Glu Thr
 245 250 255
 Gly Leu Ala Lys Leu Lys Gly Thr Ser Ala Lys Gln Trp Val Asp Tyr
 260 265 270
 Asn Gln Phe Arg Arg Glu Met Thr Leu Ala Val Leu Asp Val Val Ala
 275 280 285
 Leu Phe Pro Asn Tyr Asp Thr Ile Thr Tyr Pro Ile Glu Thr Lys Ala
 290 295 300
 Gln Leu Thr Arg Glu Val Tyr Thr Asp Pro Leu Gly Ala Val Asn Val
 305 310 315 320
 Ser Ser Ile Gly Ser Trp Tyr Asp Lys Ala Pro Ser Phe Gly Val Ile
 325 330 335
 Glu Ser Ser Val Ile Arg Pro Pro His Val Phe Asp Tyr Ile Thr Gly
 340 345 350
 Leu Thr Val Tyr Thr Gln Ser Arg Ser Ile Ser Ser Ala Arg Tyr Ile
 355 360 365
 Arg His Trp Ala Gly His Gln Ile Ser Tyr His Arg Val Ser Arg Gly
 370 375 380
 Ser Asn Leu Gln Gln Met Tyr Gly Thr Asn Gln Asn Leu His Ser Thr
 385 390 395 400

Ser Thr Phe Asp Phe Thr Asn Tyr Asp Ile Tyr Lys Thr Leu Ser Lys
 405 410 415
 Asp Ala Val Leu Leu Asp Ile Val Tyr Pro Gly Tyr Thr Tyr Ile Phe
 420 425 430
 Phe Gly Met Pro Glu Val Glu Phe Met Val Asn Gln Leu Asn Asn
 435 440 445
 Thr Arg Lys Thr Leu Lys Tyr Asn Pro Val Ser Lys Asp Ile Ile Ala
 450 455 460
 Ser Thr Arg Asp Ser Glu Leu Glu Leu Pro Pro Glu Thr Ser Asp Gln
 465 470 475 480
 Pro Asn Tyr Glu Ser Tyr Ser His Arg Leu Cys His Ile Thr Ser Ile
 485 490 495
 Pro Ala Thr Gly Asn Thr Thr Gly Leu Val Pro Val Phe Ser Trp Thr
 500 505 510
 His Arg Ser Ala Asp Leu Asn Asn Thr Ile Tyr Ser Asp Lys Ile Thr
 515 520 525
 Gln Ile Pro Ala Val Lys Cys Trp Asp Asn Leu Pro Phe Val Pro Val
 530 535 540
 Val Lys Gly Pro Gly His Thr Gly Gly Asp Leu Leu Gln Tyr Asn Arg
 545 550 555 560
 Ser Thr Gly Ser Val Gly Thr Leu Phe Leu Ala Arg Tyr Gly Leu Ala
 565 570 575
 Leu Glu Lys Ala Gly Lys Tyr Arg Val Arg Leu Arg Tyr Ala Thr Asp
 580 585 590
 Ala Asp Ile Val Leu His Val Asn Asp Ala Gln Ile Gln Met Pro Lys
 595 600 605
 Thr Met Asn Pro Gly Glu Asp Leu Thr Ser Lys Thr Phe Lys Val Ala
 610 615 620
 Asp Ala Ile Thr Thr Val Asn Leu Ala Thr Asp Ser Ser Val Ala Val
 625 630 635 640
 Lys His Asn Leu Gly Glu Asp Pro Asn Ser Thr Leu Ser Gly Ile Val
 645 650 655
 Tyr Val Asp Arg Ile Glu Phe Ile Pro Val Asp Glu Thr Tyr Glu Ala
 660 665 670
 Glu

<210> 95
 <211> 5
 <212> PRT
 <213> Bacillus thuringiensis (mutated)

<400> 95
 Phe Arg Ser Arg Gly
 1 5

<210> 96
 <211> 11
 <212> PRT
 <213> Bacillus thuringiensis (mutated)

<400> 96
 Phe Arg Ser Arg Gly Phe Arg Ser Arg Gly Pro
 1 5 10

<210> 97
 <211> 4
 <212> PRT
 <213> Bacillus thuringiensis (mutated)

<400> 97
 Phe Arg Arg Gly
 1

<210> 98
 <211> 8
 <212> PRT
 <213> Bacillus thuringiensis (mutated)

<400> 98
 Phe Arg Arg Gly Phe Arg Arg Gly
 1 5

<210> 99
 <211> 21
 <212> PRT
 <213> Bacillus thuringiensis

<400> 99
 Ile Thr Thr Leu Asn Leu Ala Thr Asp Ser Ser Leu Ala Leu Lys His
 1 5 10 15
 Asn Leu Gly Glu Asp
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<210> 100
 <211> 21
 <212> PRT
 <213> Bacillus thuringiensis (mutated)

<400> 100
 Ile Thr Thr Leu Asn Leu Ala Thr Asp Ser Ser Leu Ala Leu Lys His
 1 5 10 15
 Asn Val Gly Glu Asp
 20

<210> 101
 <211> 21
 <212> PRT
 <213> Bacillus thuringiensis (mutated)

<400> 101
 Ile Thr Thr Leu Asn Leu Ala Thr Asp Ser Ser Leu Ala Val Lys His
 1 5 10 15
 Asn Val Gly Glu Asp
 20

<210> 102
 <211> 21
 <212> PRT
 <213> *Bacillus thuringiensis* (mutated)

<400> 102
 Ile Thr Thr Val Asn Leu Ala Thr Asp Ser Ser Val Ala Val Lys His
 1 5 10 15
 Asn Leu Gly Glu Asp
 20

<210> 103
 <211> 21
 <212> PRT
 <213> *Bacillus thuringiensis* (mutated)

<400> 103
 Ile Thr Thr Val Asn Leu Ala Thr Asp Ser Ser Val Ala Val Lys His
 1 5 10 15
 Asn Val Gly Glu Asp
 20

<210> 104
 <211> 12
 <212> PRT
 <213> *Bacillus thuringiensis*

<400> 104
 Asp Tyr Lys Asp Tyr Leu Lys Met Ser Ala Gly Asn
 1 5 10

<210> 105
 <211> 12
 <212> PRT
 <213> *Bacillus thuringiensis* (mutated)

<400> 105
 Asp Tyr Lys Asp Tyr Ala Val Gly Ser Ala Gly Asn
 1 5 10

<210> 106
 <211> 8
 <212> PRT
 <213> *Bacillus thuringiensis*

<400> 106
 Ile Asn Asn Tyr Tyr Asp Arg Gln
 1 5

<210> 107
 <211> 8
 <212> PRT

<213> Bacillus thuringiensis (mutated)

<400> 107

Ile Asn Asn Val Val Asp Arg Gln
1 5

<210> 108

<211> 13

<212> PRT

<213> Bacillus thuringiensis

<400> 108

Asn Tyr Asp Thr Arg Thr Tyr Pro Met Glu Thr Lys Ala
1 5 10

<210> 109

<211> 13

<212> PRT

<213> Bacillus thuringiensis (mutated)

<400> 109

Asn Tyr Asp Thr Ile Thr Tyr Pro Ile Glu Thr Lys Ala
1 5 10

<210> 110

<211> 8

<212> PRT

<213> Bacillus thuringiensis (mutated)

<400> 110

Asn Gly Ser Arg Asn Gly Ser Arg
1 5

<210> 111

<211> 10

<212> PRT

<213> Bacillus thuringiensis (mutated)

<400> 111

Pro Phe Arg Arg Leu Lys Met Phe Phe Ala
1 5 10

<210> 112

<211> 10

<212> PRT

<213> Bacillus thuringiensis (mutated)

<400> 112

Phe Arg Ser Arg Gly Phe Arg Ser Arg Gly
1 5 10

<210> 113
 <211> 12
 <212> PRT
 <213> *Bacillus thuringiensis* (mutated)

 <400> 113
 Phe Arg Ser Arg Gly Ser Leu Asn Gly Ser Arg Pro
 1 5 10

 <210> 114
 <211> 9
 <212> PRT
 <213> *Bacillus thuringiensis*

 <400> 114
 Asn Pro Asn Gly Ser Arg Ala Leu Arg
 1 5

 <210> 115
 <211> 13
 <212> PRT
 <213> *Bacillus thuringiensis* (mutated)

 <400> 115
 Asn Pro Asn Gly Ser Arg Asn Gly Ser Arg Ala Leu Arg
 1 5 10

 <210> 116
 <211> 13
 <212> PRT
 <213> *Bacillus thuringiensis* (mutated)

 <400> 116
 Asn Pro Phe Arg Arg Gly Phe Arg Arg Gly Ala Leu Arg
 1 5 10

 <210> 117
 <211> 5
 <212> PRT
 <213> *Bacillus thuringiensis* (mutated)

 <400> 117
 Phe Arg Ser Arg Gln
 1 5

 <210> 118
 <211> 1173
 <212> DNA
 <213> *Pentaclethra macroloba* (mutated)

 <220>
 <221> CDS

<222> (1)...(1173)

<400> 118

atg gct gat gtg gca ggc tcc aca ggt gcg gga gct tct aaa gat gga	48
Met Ala Asp Val Ala Gly Ser Thr Gly Ala Gly Ala Ser Lys Asp Gly	
1 5 10 15	
aac tta gtc aca gtt ctt gcc att gat gga ggt ggt atc aga gga att	96
Asn Leu Val Thr Val Leu Ala Ile Asp Gly Gly Gly Ile Arg Gly Ile	
20 25 30	
atc ccc gga gtt att ctc aaa caa cta gaa gct act ctt cag aga tgg	144
Ile Pro Gly Val Ile Leu Lys Gln Leu Glu Ala Thr Leu Gln Arg Trp	
35 40 45	
gac tca agt gca aga cta gca gag tat ttt gat gtg gtt gcc ggg acg	192
Asp Ser Ser Ala Arg Leu Ala Glu Tyr Phe Asp Val Val Ala Gly Thr	
50 55 60	
gtc act gga ggg att ata act gcc att cta act gcc ccg gac cca caa	240
Val Thr Gly Gly Ile Ile Thr Ala Ile Leu Thr Ala Pro Asp Pro Gln	
65 70 75 80	
aac aag gac cgt cct ttg tat gct gcc gaa gaa att atc gac ttc tac	288
Asn Lys Asp Arg Pro Leu Tyr Ala Ala Glu Glu Ile Ile Asp Phe Tyr	
85 90 95	
ata gag cat ggt cct tcc att ttt aat aaa tcc acc gcc tgc tcg ttg	336
Ile Glu His Gly Pro Ser Ile Phe Asn Lys Ser Thr Ala Cys Ser Leu	
100 105 110	
cct ggt atc ttt tgt cca aag tat gat ggg aag tat tta caa gaa ata	384
Pro Gly Ile Phe Cys Pro Lys Tyr Asp Gly Lys Tyr Leu Gln Glu Ile	
115 120 125	
ata agc cag aaa ttg aat gaa aca cta cta gac cag aca aca aca aat	432
Ile Ser Gln Lys Leu Asn Glu Thr Leu Leu Asp Gln Thr Thr Thr Asn	
130 135 140	
gtt gtt atc cct tcc ttc gac atc aag ctt ctt cgt cca acc ata ttc	480
Val Val Ile Pro Ser Phe Asp Ile Lys Leu Leu Arg Pro Thr Ile Phe	
145 150 155 160	
tca act ttc aag tta gag gaa gtt cct gag tta aat gtc aaa ctc tcc	528
Ser Thr Phe Lys Leu Glu Glu Val Pro Glu Leu Asn Val Lys Leu Ser	
165 170 175	
gat gta tgc atg gga act tca gca gca cca atc gta ttt cct ccc tat	576
Asp Val Cys Met Gly Thr Ser Ala Ala Pro Ile Val Phe Pro Pro Tyr	
180 185 190	
tat ttc aag cat gga gat act gaa ttc aat ctc gtt gat ggt gca atc	624
Tyr Phe Lys His Gly Asp Thr Glu Phe Asn Leu Val Asp Gly Ala Ile	
195 200 205	
atc gct gat att ccg gcc ccg gtt gct ctc agc gag gtg ctc cag caa	672
Ile Ala Asp Ile Pro Ala Pro Val Ala Leu Ser Glu Val Leu Gln Gln	

210	215	220	
gaa aaa tac aag aat aaa gaa atc ctt ttg ctg tct ata gga act gga			720
Glu Lys Tyr Lys Asn Lys Glu Ile Leu Leu Leu Ser Ile Gly Thr Gly			
225	230	235	240
ggt gta aaa cct ggt gag ggt tat tct gct aat cgt act tgg act att			768
Val Val Lys Pro Gly Glu Gly Tyr Ser Ala Asn Arg Thr Trp Thr Ile			
	245	250	255
ttc gat tgg agt agt gaa act tta atc ggg ctt atg ggt cat gga acg			816
Phe Asp Trp Ser Ser Glu Thr Leu Ile Gly Leu Met Gly His Gly Thr			
	260	265	270
aga gcc atg tct gat tat tac gtt ggc tca cat ttc aaa gcc ctt caa			864
Arg Ala Met Ser Asp Tyr Tyr Val Gly Ser His Phe Lys Ala Leu Gln			
	275	280	285
ccc cag aat aac tac ctc cga att cag gaa tac gat tta gat ccg gca			912
Pro Gln Asn Asn Tyr Leu Arg Ile Gln Glu Tyr Asp Leu Asp Pro Ala			
	290	295	300
ctg gaa agc att gat gat gct tca acg gaa aac atg gag aat ctg gaa			960
Leu Glu Ser Ile Asp Asp Ala Ser Thr Glu Asn Met Glu Asn Leu Glu			
305	310	315	320
aag gta gga cag agt ttg ttg aac gaa cca gtt aaa agg atg aat ctg			1008
Lys Val Gly Gln Ser Leu Leu Asn Glu Pro Val Lys Arg Met Asn Leu			
	325	330	335
aat act ttt gtc gtt gaa gaa aca ggt gaa ggt acc aat gca gaa gct			1056
Asn Thr Phe Val Val Glu Glu Thr Gly Glu Gly Thr Asn Ala Glu Ala			
	340	345	350
tta gac agg ctg gct cag att ctt tat gaa gaa aag att act cgt ggt			1104
Leu Asp Arg Leu Ala Gln Ile Leu Tyr Glu Glu Lys Ile Thr Arg Gly			
	355	360	365
ctc gga aag ata tct ttg gaa gtg gat aac att gat cca tat act gaa			1152
Leu Gly Lys Ile Ser Leu Glu Val Asp Asn Ile Asp Pro Tyr Thr Glu			
	370	375	380
cgt gtt agg aaa ctg cta ttc			1173
Arg Val Arg Lys Leu Leu Phe			
385	390		

<210> 119

<211> 391

<212> PRT

<213> Pentaclethra macroloba (mutated)

<400> 119

Met	Ala	Asp	Val	Ala	Gly	Ser	Thr	Gly	Ala	Gly	Ala	Ser	Lys	Asp	Gly
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Asn	Leu	Val	Thr	Val	Leu	Ala	Ile	Asp	Gly	Gly	Gly	Ile	Arg	Gly	Ile
			20					25					30		

Ile	Pro	Gly	Val	Ile	Leu	Lys	Gln	Leu	Glu	Ala	Thr	Leu	Gln	Arg	Trp
		35					40					45			
Asp	Ser	Ser	Ala	Arg	Leu	Ala	Glu	Tyr	Phe	Asp	Val	Val	Ala	Gly	Thr
	50				55					60					
Val	Thr	Gly	Gly	Ile	Ile	Thr	Ala	Ile	Leu	Thr	Ala	Pro	Asp	Pro	Gln
65				70					75					80	
Asn	Lys	Asp	Arg	Pro	Leu	Tyr	Ala	Ala	Glu	Glu	Ile	Ile	Asp	Phe	Tyr
			85						90				95		
Ile	Glu	His	Gly	Pro	Ser	Ile	Phe	Asn	Lys	Ser	Thr	Ala	Cys	Ser	Leu
		100						105					110		
Pro	Gly	Ile	Phe	Cys	Pro	Lys	Tyr	Asp	Gly	Lys	Tyr	Leu	Gln	Glu	Ile
	115						120					125			
Ile	Ser	Gln	Lys	Leu	Asn	Glu	Thr	Leu	Leu	Asp	Gln	Thr	Thr	Thr	Asn
	130					135					140				
Val	Val	Ile	Pro	Ser	Phe	Asp	Ile	Lys	Leu	Leu	Arg	Pro	Thr	Ile	Phe
145					150					155					160
Ser	Thr	Phe	Lys	Leu	Glu	Glu	Val	Pro	Glu	Leu	Asn	Val	Lys	Leu	Ser
			165						170					175	
Asp	Val	Cys	Met	Gly	Thr	Ser	Ala	Ala	Pro	Ile	Val	Phe	Pro	Pro	Tyr
		180						185					190		
Tyr	Phe	Lys	His	Gly	Asp	Thr	Glu	Phe	Asn	Leu	Val	Asp	Gly	Ala	Ile
	195					200						205			
Ile	Ala	Asp	Ile	Pro	Ala	Pro	Val	Ala	Leu	Ser	Glu	Val	Leu	Gln	Gln
	210					215					220				
Glu	Lys	Tyr	Lys	Asn	Lys	Glu	Ile	Leu	Leu	Leu	Ser	Ile	Gly	Thr	Gly
225				230						235					240
Val	Val	Lys	Pro	Gly	Glu	Gly	Tyr	Ser	Ala	Asn	Arg	Thr	Trp	Thr	Ile
			245						250					255	
Phe	Asp	Trp	Ser	Ser	Glu	Thr	Leu	Ile	Gly	Leu	Met	Gly	His	Gly	Thr
		260						265					270		
Arg	Ala	Met	Ser	Asp	Tyr	Tyr	Val	Gly	Ser	His	Phe	Lys	Ala	Leu	Gln
	275						280					285			
Pro	Gln	Asn	Asn	Tyr	Leu	Arg	Ile	Gln	Glu	Tyr	Asp	Leu	Asp	Pro	Ala
	290				295						300				
Leu	Glu	Ser	Ile	Asp	Asp	Ala	Ser	Thr	Glu	Asn	Met	Glu	Asn	Leu	Glu
305			310							315					320
Lys	Val	Gly	Gln	Ser	Leu	Leu	Asn	Glu	Pro	Val	Lys	Arg	Met	Asn	Leu
			325						330					335	
Asn	Thr	Phe	Val	Val	Glu	Glu	Thr	Gly	Glu	Gly	Thr	Asn	Ala	Glu	Ala
		340						345					350		
Leu	Asp	Arg	Leu	Ala	Gln	Ile	Leu	Tyr	Glu	Glu	Lys	Ile	Thr	Arg	Gly
	355					360						365			
Leu	Gly	Lys	Ile	Ser	Leu	Glu	Val	Asp	Asn	Ile	Asp	Pro	Tyr	Thr	Glu
	370					375					380				
Arg	Val	Arg	Lys	Leu	Leu	Phe									
385					390										

<210> 120
 <211> 1173
 <212> DNA
 <213> Pentaclethra macroloba (mutated)

 <220>
 <221> CDS
 <222> (1)...(1173)

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<400> 120
atg gct gat gtg gca ggc tcc aca ggt gcg cat gct tct aaa gat gga 48
Met Ala Asp Val Ala Gly Ser Thr Gly Ala His Ala Ser Lys Asp Gly
1 5 10 15

aac tta gtc aca gtt ctt gcc att gat gga ggt ggt atc aga gga att 96
Asn Leu Val Thr Val Leu Ala Ile Asp Gly Gly Gly Ile Arg Gly Ile
20 25 30

atc ccc gga gtt att ctc aaa caa cta gaa gct act ctt cag aga tgg 144
Ile Pro Gly Val Ile Leu Lys Gln Leu Glu Ala Thr Leu Gln Arg Trp
35 40 45

gac tca agt gca aga cta gca gag tat ttt gat gtg gtt gcc ggg acg 192
Asp Ser Ser Ala Arg Leu Ala Glu Tyr Phe Asp Val Val Ala Gly Thr
50 55 60

gtc act gga ggg att ata act gcc att cta act gcc ccg gac cca caa 240
Val Thr Gly Gly Ile Ile Thr Ala Ile Leu Thr Ala Pro Asp Pro Gln
65 70 75 80

aac aag gac cgt cct ttg tat gct gcc gaa gaa att atc gac ttc tac 288
Asn Lys Asp Arg Pro Leu Tyr Ala Ala Glu Glu Ile Ile Asp Phe Tyr
85 90 95

ata gag cat ggt cct tcc att ttt aat aaa tcc acc gcc tgc tcg ttg 336
Ile Glu His Gly Pro Ser Ile Phe Asn Lys Ser Thr Ala Cys Ser Leu
100 105 110

cct ggt atc ttt tgt cca aag tat gat ggg aag tat tta caa gaa ata 384
Pro Gly Ile Phe Cys Pro Lys Tyr Asp Gly Lys Tyr Leu Gln Glu Ile
115 120 125

ata agc cag aaa ttg aat gaa aca cta cta gac cag aca aca aca aat 432
Ile Ser Gln Lys Leu Asn Glu Thr Leu Leu Asp Gln Thr Thr Thr Asn
130 135 140

gtt gtt atc cct tcc ttc gac atc aag ctt ctt cgt cca acc ata ttc 480
Val Val Ile Pro Ser Phe Asp Ile Lys Leu Leu Arg Pro Thr Ile Phe
145 150 155 160

tca act ttc aag tta gag gaa gtt cct gag tta aat gtc aaa ctc tcc 528
Ser Thr Phe Lys Leu Glu Glu Val Pro Glu Leu Asn Val Lys Leu Ser
165 170 175

gat gta tgc atg gga act tca gca gca cca atc gta ttt cct ccc tat 576
Asp Val Cys Met Gly Thr Ser Ala Ala Pro Ile Val Phe Pro Pro Tyr
180 185 190

tat ttc aag cat gga gat act gaa ttc aat ctc gtt gat ggt gca atc 624
Tyr Phe Lys His Gly Asp Thr Glu Phe Asn Leu Val Asp Gly Ala Ile
195 200 205

atc gct gat att ccg gcc ccg gtt gct ctc agc gag gtg ctc cag caa 672
Ile Ala Asp Ile Pro Ala Pro Val Ala Leu Ser Glu Val Leu Gln Gln
210 215 220

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gaa aaa tac aag aat aaa gaa atc ctt ttg ctg tct ata gga act gga	720
Glu Lys Tyr Lys Asn Lys Glu Ile Leu Leu Leu Ser Ile Gly Thr Gly	
225 230 235 240	
ggt gta aaa cct ggt gag ggt tat tct gct aat cgt act tgg act att	768
Val Val Lys Pro Gly Glu Gly Tyr Ser Ala Asn Arg Thr Trp Thr Ile	
245 250 255	
ttc gat tgg agt agt gaa act tta atc ggg ctt atg ggt cat gga acg	816
Phe Asp Trp Ser Ser Glu Thr Leu Ile Gly Leu Met Gly His Gly Thr	
260 265 270	
aga gcc atg tct gat tat tac gtt ggc tca cat ttc aaa gcc ctt caa	864
Arg Ala Met Ser Asp Tyr Tyr Val Gly Ser His Phe Lys Ala Leu Gln	
275 280 285	
ccc cag aat aac tac ctc cga att cag gaa tac gat tta gat ccg gca	912
Pro Gln Asn Asn Tyr Leu Arg Ile Gln Glu Tyr Asp Leu Asp Pro Ala	
290 295 300	
ctg gaa agc att gat gat gct tca acg gaa aac atg gag aat ctg gaa	960
Leu Glu Ser Ile Asp Asp Ala Ser Thr Glu Asn Met Glu Asn Leu Glu	
305 310 315 320	
aag gta gga cag agt ttg ttg aac gaa cca gtt aaa agg atg aat ctg	1008
Lys Val Gly Gln Ser Leu Leu Asn Glu Pro Val Lys Arg Met Asn Leu	
325 330 335	
aat act ttt gtc gtt gaa gaa aca ggt gaa ggt acc aat gca gaa gct	1056
Asn Thr Phe Val Val Glu Glu Thr Gly Glu Gly Thr Asn Ala Glu Ala	
340 345 350	
tta gac agg ctg gct cag att ctt tat gaa gaa aag att act cgt ggt	1104
Leu Asp Arg Leu Ala Gln Ile Leu Tyr Glu Glu Lys Ile Thr Arg Gly	
355 360 365	
ctc gga aag ata tct ttg gaa gtg gat aac att gat cca tat act gaa	1152
Leu Gly Lys Ile Ser Leu Glu Val Asp Asn Ile Asp Pro Tyr Thr Glu	
370 375 380	
cgt gtt agg aaa ctg cta ttc	1173
Arg Val Arg Lys Leu Leu Phe	
385 390	

<210> 121

<211> 391

<212> PRT

<213> Pentaclethra macroloba (mutated)

<400> 121

Met Ala Asp Val Ala Gly Ser Thr Gly Ala His Ala Ser Lys Asp Gly	
1 5 10 15	
Asn Leu Val Thr Val Leu Ala Ile Asp Gly Gly Gly Ile Arg Gly Ile	
20 25 30	
Ile Pro Gly Val Ile Leu Lys Gln Leu Glu Ala Thr Leu Gln Arg Trp	
35 40 45	

Asp	Ser	Ser	Ala	Arg	Leu	Ala	Glu	Tyr	Phe	Asp	Val	Val	Ala	Gly	Thr
50						55					60				
Val	Thr	Gly	Gly	Ile	Ile	Thr	Ala	Ile	Leu	Thr	Ala	Pro	Asp	Pro	Gln
65					70					75					80
Asn	Lys	Asp	Arg	Pro	Leu	Tyr	Ala	Ala	Glu	Glu	Ile	Ile	Asp	Phe	Tyr
				85					90					95	
Ile	Glu	His	Gly	Pro	Ser	Ile	Phe	Asn	Lys	Ser	Thr	Ala	Cys	Ser	Leu
			100					105					110		
Pro	Gly	Ile	Phe	Cys	Pro	Lys	Tyr	Asp	Gly	Lys	Tyr	Leu	Gln	Glu	Ile
		115					120					125			
Ile	Ser	Gln	Lys	Leu	Asn	Glu	Thr	Leu	Leu	Asp	Gln	Thr	Thr	Thr	Asn
	130					135					140				
Val	Val	Ile	Pro	Ser	Phe	Asp	Ile	Lys	Leu	Leu	Arg	Pro	Thr	Ile	Phe
145					150					155					160
Ser	Thr	Phe	Lys	Leu	Glu	Glu	Val	Pro	Glu	Leu	Asn	Val	Lys	Leu	Ser
			165					170						175	
Asp	Val	Cys	Met	Gly	Thr	Ser	Ala	Ala	Pro	Ile	Val	Phe	Pro	Pro	Tyr
			180					185					190		
Tyr	Phe	Lys	His	Gly	Asp	Thr	Glu	Phe	Asn	Leu	Val	Asp	Gly	Ala	Ile
	195						200					205			
Ile	Ala	Asp	Ile	Pro	Ala	Pro	Val	Ala	Leu	Ser	Glu	Val	Leu	Gln	Gln
	210					215					220				
Glu	Lys	Tyr	Lys	Asn	Lys	Glu	Ile	Leu	Leu	Leu	Ser	Ile	Gly	Thr	Gly
225					230					235					240
Val	Val	Lys	Pro	Gly	Glu	Gly	Tyr	Ser	Ala	Asn	Arg	Thr	Trp	Thr	Ile
			245						250					255	
Phe	Asp	Trp	Ser	Ser	Glu	Thr	Leu	Ile	Gly	Leu	Met	Gly	His	Gly	Thr
			260					265					270		
Arg	Ala	Met	Ser	Asp	Tyr	Tyr	Val	Gly	Ser	His	Phe	Lys	Ala	Leu	Gln
	275						280					285			
Pro	Gln	Asn	Asn	Tyr	Leu	Arg	Ile	Gln	Glu	Tyr	Asp	Leu	Asp	Pro	Ala
	290					295					300				
Leu	Glu	Ser	Ile	Asp	Asp	Ala	Ser	Thr	Glu	Asn	Met	Glu	Asn	Leu	Glu
305				310						315					320
Lys	Val	Gly	Gln	Ser	Leu	Leu	Asn	Glu	Pro	Val	Lys	Arg	Met	Asn	Leu
			325						330					335	
Asn	Thr	Phe	Val	Val	Glu	Glu	Thr	Gly	Glu	Gly	Thr	Asn	Ala	Glu	Ala
			340					345					350		
Leu	Asp	Arg	Leu	Ala	Gln	Ile	Leu	Tyr	Glu	Glu	Lys	Ile	Thr	Arg	Gly
	355						360					365			
Leu	Gly	Lys	Ile	Ser	Leu	Glu	Val	Asp	Asn	Ile	Asp	Pro	Tyr	Thr	Glu
	370					375					380				
Arg	Val	Arg	Lys	Leu	Leu	Phe									
385					390										

<210> 122

<211> 1173

<212> DNA

<213> Pentaclethra macroloba (mutated)

<220>

<221> CDS

<222> (1)...(1173)

<400> 122

atg gct gat gtg gca ggc tcc aca cac gcg cat gct tct aaa gat gga 48

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1				5					10					15			
aac	tta	gtc	aca	gtt	ctt	gcc	att	gat	gga	ggg	ggg	atc	aga	gga	att	96	
Asn	Leu	Val	Thr	Val	Leu	Ala	Ile	Asp	Gly	Gly	Gly	Ile	Arg	Gly	Ile		
			20					25					30				
atc	ccc	gga	gtt	att	ctc	aaa	caa	cta	gaa	gct	act	ctt	cag	aga	tgg	144	
Ile	Pro	Gly	Val	Ile	Leu	Lys	Gln	Leu	Glu	Ala	Thr	Leu	Gln	Arg	Trp		
			35				40					45					
gac	tca	agt	gca	aga	cta	gca	gag	tat	ttt	gat	gtg	gtt	gcc	ggg	acg	192	
Asp	Ser	Ser	Ala	Arg	Leu	Ala	Glu	Tyr	Phe	Asp	Val	Val	Ala	Gly	Thr		
		50				55				60							
gtc	act	gga	ggg	att	ata	act	gcc	att	cta	act	gcc	ccg	gac	cca	caa	240	
Val	Thr	Gly	Gly	Ile	Ile	Thr	Ala	Ile	Leu	Thr	Ala	Pro	Asp	Pro	Gln		
	65				70				75					80			
aac	aag	gac	cgt	cct	ttg	tat	gct	gcc	gaa	gaa	att	atc	gac	ttc	tac	288	
Asn	Lys	Asp	Arg	Pro	Leu	Tyr	Ala	Ala	Glu	Glu	Ile	Ile	Asp	Phe	Tyr		
				85				90						95			
ata	gag	cat	ggg	cct	tcc	att	ttt	aat	aaa	tcc	acc	gcc	tgc	tcg	ttg	336	
Ile	Glu	His	Gly	Pro	Ser	Ile	Phe	Asn	Lys	Ser	Thr	Ala	Cys	Ser	Leu		
			100					105					110				
cct	ggg	atc	ttt	tgt	cca	aag	tat	gat	ggg	aag	tat	tta	caa	gaa	ata	384	
Pro	Gly	Ile	Phe	Cys	Pro	Lys	Tyr	Asp	Gly	Lys	Tyr	Leu	Gln	Glu	Ile		
		115					120					125					
ata	agc	cag	aaa	ttg	aat	gaa	aca	cta	cta	gac	cag	aca	aca	aca	aat	432	
Ile	Ser	Gln	Lys	Leu	Asn	Glu	Thr	Leu	Leu	Asp	Gln	Thr	Thr	Thr	Asn		
		130				135					140						
gtt	gtt	atc	cct	tcc	ttc	gac	atc	aag	ctt	ctt	cgt	cca	acc	ata	ttc	480	
Val	Val	Ile	Pro	Ser	Phe	Asp	Ile	Lys	Leu	Leu	Arg	Pro	Thr	Ile	Phe		
	145				150				155					160			
tca	act	ttc	aag	tta	gag	gaa	gtt	cct	gag	tta	aat	gtc	aaa	ctc	tcc	528	
Ser	Thr	Phe	Lys	Leu	Glu	Glu	Val	Pro	Glu	Leu	Asn	Val	Lys	Leu	Ser		
				165					170					175			
gat	gta	tgc	atg	gga	act	tca	gca	gca	cca	atc	gta	ttt	cct	ccc	tat	576	
Asp	Val	Cys	Met	Gly	Thr	Ser	Ala	Ala	Pro	Ile	Val	Phe	Pro	Pro	Tyr		
			180				185						190				
tat	ttc	aag	cat	gga	gat	act	gaa	ttc	aat	ctc	gtt	gat	ggg	gca	atc	624	
Tyr	Phe	Lys	His	Gly	Asp	Thr	Glu	Phe	Asn	Leu	Val	Asp	Gly	Ala	Ile		
		195				200						205					
atc	gct	gat	att	ccg	gcc	ccg	gtt	gct	ctc	agc	gag	gtg	ctc	cag	caa	672	
Ile	Ala	Asp	Ile	Pro	Ala	Pro	Val	Ala	Leu	Ser	Glu	Val	Leu	Gln	Gln		
		210				215					220						
gaa	aaa	tac	aag	aat	aaa	gaa	atc	ctt	ttg	ctg	tct	ata	gga	act	gga	720	
Glu	Lys	Tyr	Lys	Asn	Lys	Glu	Ile	Leu	Leu	Leu	Ser	Ile	Gly	Thr	Gly		

225	230	235	240	
gtt gta aaa cct ggt gag ggt tat tct gct aat cgt act tgg act att				768
Val Val Lys Pro Gly Glu Gly Tyr Ser Ala Asn Arg Thr Trp Thr Ile				
	245	250	255	
ttc gat tgg agt agt gaa act tta atc ggg ctt atg ggt cat gga acg				816
Phe Asp Trp Ser Ser Glu Thr Leu Ile Gly Leu Met Gly His Gly Thr				
	260	265	270	
aga gcc atg tct gat tat tac gtt ggc tca cat ttc aaa gcc ctt caa				864
Arg Ala Met Ser Asp Tyr Tyr Val Gly Ser His Phe Lys Ala Leu Gln				
	275	280	285	
ccc cag aat aac tac ctc cga att cag gaa tac gat tta gat ccg gca				912
Pro Gln Asn Asn Tyr Leu Arg Ile Gln Glu Tyr Asp Leu Asp Pro Ala				
	290	295	300	
ctg gaa agc att gat gat gct tca acg gaa aac atg gag aat ctg gaa				960
Leu Glu Ser Ile Asp Asp Ala Ser Thr Glu Asn Met Glu Asn Leu Glu				
	305	310	315	320
aag gta gga cag agt ttg ttg aac gaa cca gtt aaa agg atg aat ctg				1008
Lys Val Gly Gln Ser Leu Leu Asn Glu Pro Val Lys Arg Met Asn Leu				
	325	330	335	
aat act ttt gtc gtt gaa gaa aca ggt gaa ggt acc aat gca gaa gct				1056
Asn Thr Phe Val Val Glu Glu Thr Gly Glu Gly Thr Asn Ala Glu Ala				
	340	345	350	
tta gac agg ctg gct cag att ctt tat gaa gaa aag att act cgt ggt				1104
Leu Asp Arg Leu Ala Gln Ile Leu Tyr Glu Glu Lys Ile Thr Arg Gly				
	355	360	365	
ctc gga aag ata tct ttg gaa gtg gat aac att gat cca tat act gaa				1152
Leu Gly Lys Ile Ser Leu Glu Val Asp Asn Ile Asp Pro Tyr Thr Glu				
	370	375	380	
cgt gtt agg aaa ctg cta ttc				1173
Arg Val Arg Lys Leu Phe				
	385	390		

<210> 123

<211> 391

<212> PRT

<213> *Pentaclethra macroloba* (mutated)

<400> 123

Met Ala Asp Val Ala Gly Ser Thr His Ala His Ala Ser Lys Asp Gly				
1	5	10	15	
Asn Leu Val Thr Val Leu Ala Ile Asp Gly Gly Gly Ile Arg Gly Ile				
	20	25	30	
Ile Pro Gly Val Ile Leu Lys Gln Leu Glu Ala Thr Leu Gln Arg Trp				
	35	40	45	
Asp Ser Ser Ala Arg Leu Ala Glu Tyr Phe Asp Val Val Ala Gly Thr				
	50	55	60	

Val	Thr	Gly	Gly	Ile	Ile	Thr	Ala	Ile	Leu	Thr	Ala	Pro	Asp	Pro	Gln
65				70					75					80	
Asn	Lys	Asp	Arg	Pro	Leu	Tyr	Ala	Ala	Glu	Glu	Ile	Ile	Asp	Phe	Tyr
			85						90					95	
Ile	Glu	His	Gly	Pro	Ser	Ile	Phe	Asn	Lys	Ser	Thr	Ala	Cys	Ser	Leu
			100					105					110		
Pro	Gly	Ile	Phe	Cys	Pro	Lys	Tyr	Asp	Gly	Lys	Tyr	Leu	Gln	Glu	Ile
		115					120					125			
Ile	Ser	Gln	Lys	Leu	Asn	Glu	Thr	Leu	Leu	Asp	Gln	Thr	Thr	Thr	Asn
		130				135					140				
Val	Val	Ile	Pro	Ser	Phe	Asp	Ile	Lys	Leu	Leu	Arg	Pro	Thr	Ile	Phe
145					150				155					160	
Ser	Thr	Phe	Lys	Leu	Glu	Glu	Val	Pro	Glu	Leu	Asn	Val	Lys	Leu	Ser
			165						170					175	
Asp	Val	Cys	Met	Gly	Thr	Ser	Ala	Ala	Pro	Ile	Val	Phe	Pro	Pro	Tyr
		180					185					190			
Tyr	Phe	Lys	His	Gly	Asp	Thr	Glu	Phe	Asn	Leu	Val	Asp	Gly	Ala	Ile
		195				200						205			
Ile	Ala	Asp	Ile	Pro	Ala	Pro	Val	Ala	Leu	Ser	Glu	Val	Leu	Gln	Gln
		210				215					220				
Glu	Lys	Tyr	Lys	Asn	Lys	Glu	Ile	Leu	Leu	Leu	Ser	Ile	Gly	Thr	Gly
225				230					235					240	
Val	Val	Lys	Pro	Gly	Glu	Gly	Tyr	Ser	Ala	Asn	Arg	Thr	Trp	Thr	Ile
			245						250					255	
Phe	Asp	Trp	Ser	Ser	Glu	Thr	Leu	Ile	Gly	Leu	Met	Gly	His	Gly	Thr
		260					265					270			
Arg	Ala	Met	Ser	Asp	Tyr	Tyr	Val	Gly	Ser	His	Phe	Lys	Ala	Leu	Gln
		275				280					285				
Pro	Gln	Asn	Asn	Tyr	Leu	Arg	Ile	Gln	Glu	Tyr	Asp	Leu	Asp	Pro	Ala
		290				295				300					
Leu	Glu	Ser	Ile	Asp	Asp	Ala	Ser	Thr	Glu	Asn	Met	Glu	Asn	Leu	Glu
305				310					315					320	
Lys	Val	Gly	Gln	Ser	Leu	Leu	Asn	Glu	Pro	Val	Lys	Arg	Met	Asn	Leu
			325						330				335		
Asn	Thr	Phe	Val	Val	Glu	Glu	Thr	Gly	Glu	Gly	Thr	Asn	Ala	Glu	Ala
		340					345					350			
Leu	Asp	Arg	Leu	Ala	Gln	Ile	Leu	Tyr	Glu	Glu	Lys	Ile	Thr	Arg	Gly
		355				360					365				
Leu	Gly	Lys	Ile	Ser	Leu	Glu	Val	Asp	Asn	Ile	Asp	Pro	Tyr	Thr	Glu
		370				375					380				
Arg	Val	Arg	Lys	Leu	Leu	Phe									
385				390											

<210> 124

<211> 4

<212> PRT

<213> Artificial Sequence

<220>

<223> amino acids added to N-terminus to enhance
production of modified pentin-1 protein in a host
cell

<400> 124

Met Ala Asp Val

1

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<210> 125
<211> 15
<212> PRT
<213> Pentaclethra macroloba (mutated)

<220>
<223> sequence from modified pentin-1 protein

<400> 125
Met Ala Asp Val Ala Phe Ser Thr Gln Ala Lys Ala Ser Lys Asp
 1             5             10             15

<210> 126
<211> 30
<212> PRT
<213> Pentaclethra macroloba (mutated)

<400> 126
Met Ala Asp Val Ala Phe Ser Thr Gln Ala Lys Ala Ser Lys Asp Gly
 1             5             10             15
Asn Leu Val Thr Val Leu Ala Ile Asp Gly Gly Gly Ile Arg
      20             25             30

<210> 127
<211> 30
<212> PRT
<213> Pentaclethra macroloba (mutated)

<400> 127
Met Ala Asp Val Ala Gly Ser Thr Gly Ala Gly Ala Ser Lys Asp Gly
 1             5             10             15
Asn Leu Val Thr Val Leu Ala Ile Asp Gly Gly Gly Ile Arg
      20             25             30

<210> 128
<211> 30
<212> PRT
<213> Pentaclethra macroloba (mutated)

<400> 128
Met Ala Asp Val Ala Gly Ser Thr Gly Ala His Ala Ser Lys Asp Gly
 1             5             10             15
Asn Leu Val Thr Val Leu Ala Ile Asp Gly Gly Gly Ile Arg
      20             25             30

<210> 129
<211> 30
<212> PRT
<213> Pentaclethra macroloba (mutated)

<400> 129

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Met	Ala	Asp	Val	Ala	Gly	Ser	Thr	His	Ala	His	Ala	Ser	Lys	Asp	Gly
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Asn	Leu	Val	Thr	Val	Leu	Ala	Ile	Asp	Gly	Gly	Gly	Ile	Arg		
			20				25						30		

<210> 130
 <211> 30
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> primer

<400> 130
 gccacatcag ccatggcctt gtcgtcgtcg 30

<210> 131
 <211> 60
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> NEZ1 mutation forward primer

<400> 131
 gacaaggcca tggctgatgt ggcaggctcc acagggtgcgg gagcttctaa agatggaaac 60

<210> 132
 <211> 60
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> NEZ2 mutation forward primer

<400> 132
 gacaaggcca tggctgatgt ggcaggctcc acagggtgcgc atgcttctaa agatggaaac 60

<210> 133
 <211> 60
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> NEZ3 mutation forward primer

<400> 133
 gacaaggcca tggctgatgt ggcaggctcc acacacgcgc atgcttctaa agatggaaac 60

<210> 134
 <211> 30
 <212> DNA
 <213> Artificial Sequence

<220>
<223> modified 5' end of pentin-1 sequence

<400> 134
cgacgacgac aaggccatgg ctgatgtggc

30